

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:06 ; Search time 43.3077 Seconds
(without alignments)
71.766 Million cell updates/sec

Title: US-09-787-443A-14
Perfect score: 11
Sequence: 1 ARKTRERKSKD 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 22883

Minimum DB seq length: 11
Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

		8					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	11	100.0	11	3	AAy88542	Aay88542 NCAM Igl	
2	11	100.0	11	5	ABG69342	Abg69342 Human neu	
3	4	36.4	11	2	AAW40399	Aaw40399 NNOS bind	
4	4	36.4	11	5	ABB74475	Abb74475 DNA repai	
5	4	36.4	11	5	AAU96240	Aau96240 Class I G	
6	4	36.4	11	6	AAE34290	Aae34290 Human 5-h	
7	4	36.4	11	6	AAE34216	Aae34216 Human 5-h	
8	3	27.3	11	1	AAP40439	Aap40439 Sequence	
9	3	27.3	11	1	AAP40131	Aap40131 Clones pJ	

10	3	27.3	11	1	AAP40132	Aap40132	Clones pJ
11	3	27.3	11	1	AAP60142	Aap60142	Type 3 pe
12	3	27.3	11	1	AAP91264	Aap91264	Tissue pl
13	3	27.3	11	2	AAR06754	Aar06754	Tumour ne
14	3	27.3	11	2	AAR10931	Aar10931	Relaxin C
15	3	27.3	11	2	AAR12375	Aar12375	Human Fac
16	3	27.3	11	2	AAR22743	Aar22743	Non-A, No
17	3	27.3	11	2	AAR31357	Aar31357	Antimicro
18	3	27.3	11	2	AAR28089	Aar28089	Cell-to-c
19	3	27.3	11	2	AAR28088	Aar28088	Cell-to-c
20	3	27.3	11	2	AAR28128	Aar28128	Cell-to-c
21	3	27.3	11	2	AAR28130	Aar28130	Cell-to-c
22	3	27.3	11	2	AAR28132	Aar28132	Cell-to-c
23	3	27.3	11	2	AAR44843	Aar44843	Lactoferr
24	3	27.3	11	2	AAR32352	Aar32352	Human Fac
25	3	27.3	11	2	AAR37430	Aar37430	Promega p
26	3	27.3	11	2	AAR34421	Aar34421	Hepatitis
27	3	27.3	11	2	AAR57464	Aar57464	Lactoferr
28	3	27.3	11	2	AAR66080	Aar66080	Phosphory
29	3	27.3	11	2	AAR66072	Aar66072	Phosphory
30	3	27.3	11	2	AAR66083	Aar66083	Phosphory
31	3	27.3	11	2	AAR48537	Aar48537	Lactoferr
32	3	27.3	11	2	AAR63547	Aar63547	HT-LCF pe
33	3	27.3	11	2	AAR66534	Aar66534	Human inf
34	3	27.3	11	2	AAR70606	Aar70606	HIV(B35)A
35	3	27.3	11	2	AAR84701	Aar84701	Bovine la
36	3	27.3	11	2	AAR80266	Aar80266	Anti-para
37	3	27.3	11	2	AAR84537	Aar84537	Hepatitis
38	3	27.3	11	2	AAR64598	Aar64598	RF-1 pept
39	3	27.3	11	2	AAR87611	Aar87611	Lactoferr
40	3	27.3	11	2	AAR91854	Aar91854	Lactoferr
41	3	27.3	11	2	AAW12602	Aaw12602	SH2 bindi
42	3	27.3	11	2	AAW05350	Aaw05350	Residues
43	3	27.3	11	2	AAW05374	Aaw05374	Reverse D
44	3	27.3	11	2	AAW03991	Aaw03991	pY peptid
45	3	27.3	11	2	AAR96813	Aar96813	Human lam
46	3	27.3	11	2	AAR96812	Aar96812	N.gonorrh
47	3	27.3	11	2	AAR96834	Aar96834	N.gonorrh
48	3	27.3	11	2	AAR81803	Aar81803	E-Dex int
49	3	27.3	11	2	AAR90709	Aar90709	Residues
50	3	27.3	11	2	AAW02115	Aaw02115	Biotiny la
51	3	27.3	11	2	AAW09653	Aaw09653	Labelled
52	3	27.3	11	2	AAW25587	Aaw25587	Synthetic
53	3	27.3	11	2	AAW25586	Aaw25586	Synthetic
54	3	27.3	11	2	AAW15675	Aaw15675	Platelet
55	3	27.3	11	2	AAW22738	Aaw22738	Linking s
56	3	27.3	11	2	AAW38140	Aaw38140	Linking s
57	3	27.3	11	2	AAW39576	Aaw39576	Human Inf
58	3	27.3	11	2	AAW14038	Aaw14038	Anti-para
59	3	27.3	11	2	AAW16616	Aaw16616	Phosphoin
60	3	27.3	11	2	AAW10140	Aaw10140	Hepatitis
61	3	27.3	11	2	AAW26152	Aaw26152	Lactoferr
62	3	27.3	11	2	AAW70312	Aaw70312	Thrombus
63	3	27.3	11	2	AAW69270	Aaw69270	Haemagglu
64	3	27.3	11	2	AAW20426	Aay20426	Human mic
65	3	27.3	11	2	AAW78553	Aaw78553	SH2 domai
66	3	27.3	11	2	AAW78592	Aaw78592	SH2 domai

67	3	27.3	11	2	AAW41292	Aaw41292	Apoptosis
68	3	27.3	11	2	AAW61162	Aaw61162	IgE deriv
69	3	27.3	11	2	AAW53227	Aaw53227	Lactoferr
70	3	27.3	11	2	AAW30697	Aay30697	Apo-B100
71	3	27.3	11	2	AAW33387	Aay33387	Zinc fing
72	3	27.3	11	2	AAW03092	Aay03092	New nocic
73	3	27.3	11	2	AAW47022	Aay47022	Immunogen
74	3	27.3	11	2	AAW07983	Aay07983	Human sec
75	3	27.3	11	2	AAW67680	Aaw67680	LXXLL sig
76	3	27.3	11	2	AAW74077	Aaw74077	Fragment
77	3	27.3	11	2	AAW74135	Aaw74135	GI transp
78	3	27.3	11	2	AAW97473	Aaw97473	Antigenic
79	3	27.3	11	2	AAW97472	Aaw97472	Antigenic
80	3	27.3	11	2	AAW97476	Aaw97476	Antigenic
81	3	27.3	11	2	AAW97477	Aaw97477	Antigenic
82	3	27.3	11	2	AAW97474	Aaw97474	Antigenic
83	3	27.3	11	2	AAW97475	Aaw97475	Antigenic
84	3	27.3	11	2	AAW01172	Aay01172	Polypepti
85	3	27.3	11	2	AAW92727	Aaw92727	Human tac
86	3	27.3	11	2	AAW55306	Aay55306	CD34 anti
87	3	27.3	11	2	AAW31014	Aay31014	Non-cross
88	3	27.3	11	3	AAW89315	Aay89315	Core poly
89	3	27.3	11	3	AAW88562	Aay88562	NCAM Igl
90	3	27.3	11	3	AAW88550	Aay88550	NCAM Igl
91	3	27.3	11	3	AAW65723	Aay65723	Breast ca
92	3	27.3	11	3	AAW56541	Aay56541	Peptide S
93	3	27.3	11	3	AAW93125	Aay93125	Transform
94	3	27.3	11	3	AAW93544	Aay93544	Amino aci
95	3	27.3	11	3	AAW87052	Aay87052	Human hae
96	3	27.3	11	3	AAW59212	Aay59212	Rhamnogal
97	3	27.3	11	3	AAW81393	Aay81393	PKC-alpha
98	3	27.3	11	3	AAW54478	Aay54478	Peptide u
99	3	27.3	11	3	AAW86592	Aay86592	Telomeras
100	3	27.3	11	3	AAB29416	Aab29416	Synthetic

ALIGNMENTS

RESULT 1

AAW88542

ID AAW88542 standard; peptide; 11 AA.

XX

AC AAW88542;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Igl binding peptide #14.

XX

KW NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.
XX
PD 06-APR-2000.
XX
PF 23-SEP-1999; 99WO-DK000500.
XX
PR 29-SEP-1998; 98DK-00001232.
PR 29-APR-1999; 99DK-00000592.
XX
PA (RONN/) RONN L C B.
PA (BOCK/) BOCK E.
PA (HOLM/) HOLM A.
PA (OLSE/) OLSEN M.
PA (OSTE/) OSTERGAARD S.
PA (JENS/) JENSEN P H.
PA (POUL/) POULSEN F M.
PA (SORO/) SOROKA V.
PA (RALE/) RALETS I.
PA (BERE/) BEREZIN V.
XX
PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
PI Poulsen FM, Soroka V, Ralets I, Berezin V;
XX
DR WPI; 2000-293111/25.
XX
PT Compositions that bind neural cell adhesion molecules useful for treating
PT disorders of the nervous system and muscles e.g. Alzheimer's and
PT Parkinson's diseases.
XX
PS Example 4; Page 25; 119pp; English.
XX
CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
CC NCAM is found in three forms, two of which are transmembrane forms, while
CC the third is attached via a lipid anchor to the cell membrane. All three
CC NCAM forms have an extracellular structure consisting five immunoglobulin
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
CC terminal. The present sequence represents a peptide which binds to the
CC NCAM Ig1 domain. The peptide can be used in a compound which binds to
CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite
CC outgrowth from NCAM presenting cells, and is also capable of promoting
CC the proliferation of NCAM presenting cells. The compound may be used in
CC the treatment of normal, degenerated or damaged NCAM presenting cells.
CC The compound may in particular be used to treat diseases of the central
CC and peripheral nervous systems such as post operative nerve damage,
CC traumatic nerve damage, impaired myelination of nerve fibres, conditions
CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
CC dementias, sclerosis, nerve degeneration associated with diabetes
CC mellitus, disorders affecting the circadian clock or neuro-muscular
CC transmission and schizophrenia. Conditions affecting the muscles may also
CC be treated with the compound, such as conditions associated with impaired
CC function of neuromuscular connections (e.g. genetic or traumatic shock or
CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
CC liver and bowel may also be treated using the compound. The compound is
CC used in a prosthetic nerve guide, and also to stimulate the ability to
CC learn, and to stimulate the memory of a subject
XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARKTRERKSKD 11
| | | | | | | | | |
Db 1 ARKTRERKSKD 11

RESULT 2

ABG69342

ID ABG69342 standard; peptide; 11 AA.

XX

AC ABG69342;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human neural cell adhesion molecule (NCAM) peptide #14.

XX

KW Human; neural cell adhesion molecule; NCAM; heart muscle cell survival;

KW acute myocardial infarction; central nervous system disorder; stroke;

KW peripheral nervous system disorder; postoperative nerve damage;

KW traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;

KW postischaemic damage; multiinfarct dementia; multiple sclerosis;

KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;

KW Alzheimer's disease; Parkinson's disease;

KW Huntington's disease. atrophic muscle disorder; gonad degeneration;

KW nephrosis.

XX

OS Homo sapiens.

XX

PN WO200247719-A2.

XX

PD 20-JUN-2002.

XX

PF 12-DEC-2001; 2001WO-DK000822.

XX

PR 12-DEC-2000; 2000DK-00001863.

XX

PA (ENKA-) ENKAM PHARM AS.

XX

PI Bock E, Berezin V, Kohler LB;

XX

DR WPI; 2002-583473/62.

XX

PT Use of a compound comprising a peptide of neural cell adhesion molecule,

PT in the preparation of medicament for preventing death of cells presenting

PT NCAM or NCAM ligand and treating central nervous system diseases.

XX

PS Disclosure; Page 16; 57pp; English.

XX

CC The invention relates to use of a compound (I) comprising a peptide which

CC comprises at least 5 contiguous amino acid residues of a sequence of the

CC neural cell adhesion molecule (NCAM), its fragment, variant or its mimic,

CC for the preparation of a medicament for preventing death of cells

CC presenting the NCAM or an NCAM ligand. (I) is useful in the preparation
 CC of a medicament for preventing death of cells presenting the NCAM or an
 CC NCAM ligand. The medicament is for the stimulation of the survival of
 CC heart muscle cells, such as survival after acute myocardial infarction.
 CC The medicament is for the treatment of diseases or conditions of the
 CC central and peripheral nervous system, such as postoperative nerve
 CC damage, traumatic nerve damage, e.g. resulting from spinal cord injury,
 CC impaired myelination of nerve fibres, postischaemic damage, e.g.
 CC resulting from a stroke, multiinfarct dementia, multiple sclerosis, nerve
 CC degeneration associated with diabetes mellitus, neuro-muscular
 CC degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease and
 CC Huntington's disease. The medicament is for the treatment of diseases or
 CC conditions of the muscles including conditions with impaired function of
 CC neuro-muscular connections, such as genetic or traumatic atrophic muscle
 CC disorders, and for the treatment of diseases or conditions of various
 CC organs, such as degenerative conditions of the gonads, pancreas (e.g.
 CC diabetes mellitus type I and II) and kidney (e.g. nephrosis). ABG69329-
 CC ABG69352 represent human NCAM peptides of the invention
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARKTRERKSKD 11
 |||||
 Db 1 ARKTRERKSKD 11

RESULT 3

AAW40399

ID AAW40399 standard; protein; 11 AA.

XX

AC AAW40399;

XX

DT 17-OCT-2003 (revised)

DT 23-JUL-1998 (first entry)

XX

DE NNOS binding peptide #1.

XX

KW Nitric oxide synthase; endothelial; ENOS; INOS; inducible; NNOS;

KW neuronal; calmodulin; brain damage; shock; autoimmune disease;

KW inflammatory condition; multiple sclerosis; diabetes; dementia;

KW dysplasia; cancer; infectious disease; cytotoxic; hypertension;

KW atherosclerosis; asthma; detection; screening.

XX

OS unidentified.

XX

PN WO9802555-A1.

XX

PD 22-JAN-1998.

XX

PF 10-JUL-1997; 97WO-US012568.

XX

PR 12-JUL-1996; 96US-00679006.

XX

PA (SALE/) SALERNO J C.
XX
PI Salerno JC;
XX
DR WPI; 1998-110601/10.
XX
PT New modulators of nitric oxide synthase - used for treating e.g. toxic
PT shock, auto-immune disease, inflammatory disease, diabetes, hypertension,
PT infections or cancer.
XX
PS Claim 14; Page 41; 78pp; English.
XX

CC This sequence represents a peptide which binds adjacent to the calmodulin
CC binding site of neuronal nitric oxide synthase (NNOS). This peptide is
CC used in a novel method which identifies an agent which inhibits nitric
CC oxide synthase (NOS) by blocking calmodulin (CAM) activation of the NOS.
CC Such agents which modulate NOS activity can be used to treat a disease or
CC condition associated with nitric oxide production. Agents which inhibit
CC neuronal NOS (NNOS) can be used to prevent brain damage in conditions
CC involving cerebral ischaemia or reperfusion injury, such as head trauma.
CC Agents which decrease the activity of inducible NOS (INOS) can be used to
CC treat a condition modulated by production of NO by INOS, such as septic
CC shock, toxic shock, autoimmune disease such as rheumatoid arthritis,
CC inflammatory conditions such as inflammatory bowel disease, multiple
CC sclerosis, diabetes, or to combat dementia, immune system destruction,
CC and/or physical deterioration in individuals infected with the AIDS
CC virus. Agents which activate INOS can be used to treat disease relating
CC to dysplasia, cancer, or infectious disease. Activation of INOS can
CC produce cytotoxic levels of NO which would aid in the elimination of
CC dysplastic or cancerous tissue, or aid in the control of infectious
CC agents such as viruses, microbes, or other parasites. Agents which
CC increase the activity of endothelial NOS (ENOS) can be used to treat a
CC condition modulated by production of NO by ENOS such as hypertension,
CC atherosclerosis or acute asthma. An agent which activates ENOS or NNOS in
CC the corpus cavernosa can be used for treating male erectile dysfunction.
CC The products and methods can also be used for detection and drug
CC screening. (Updated on 17-OCT-2003 to standardise OS field)

XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ERKS 9
| | | |
Db 3 ERKS 6

RESULT 4
ABB74475
ID ABB74475 standard; peptide; 11 AA.
XX
AC ABB74475;
XX
DT 18-APR-2002 (first entry)
XX

DE DNA repair protein nuclear localisation signal peptide SEQ ID NO:239.
XX
KW Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene;
KW liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;
KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;
KW breast carcinoma; prostate carcinoma.
XX
OS Eukaryota.
XX
PN WO200193836-A2.
XX
PD 13-DEC-2001.
XX
PF 08-JUN-2001; 2001WO-US018657.
XX
PR 09-JUN-2000; 2000US-0210925P.
XX
PA (BOUL/) BOULIKAS T.
XX
PI Boulikas T;
XX
DR WPI; 2002-164295/21.
XX
PT Encapsulation of plasmid DNA (Lipogenes) and therapeutic agents with
PT nuclear localization signal/fusogenic peptide conjugates into targeted
PT liposome complexes.
XX
PS Claim 14; Page 69; 107pp; English.
XX
CC The present invention describes a method for producing micelles with
CC entrapped therapeutic agents. The method comprises: (1) combining
CC negatively charged agent with a cationic lipid in a ratio where 30-90 %
CC of the negatively charged atoms are neutralised by positive charges on
CC lipid molecules to form an electrostatic micelle complex in 20-80 %
CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-
CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing
CC micelles with entrapped therapeutic agents. Also described is a method
CC for delivering a therapeutic agent in vivo, comprising the administration
CC of the micelle. ABB74256 to ABB74858 represent specifically claimed
CC nuclear localisation signal (NLS) peptides for use in the method as the
CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic
CC and antitumour activities. The peptide-lipid-polynucleotide complexes
CC produced are useful for inhibiting the progression of neoplastic
CC diseases. The invention relates to the field of gene therapy and is
CC directed toward methods for producing peptide-lipid-polynucleotide
CC complexes suitable for delivery of polynucleotides. The encapsulated
CC molecules display therapeutic efficacy in eradicating solid tumours
CC including but not limited to breast carcinoma or prostate carcinoma.
CC ABB74235 to ABB74255 are used in the exemplification of the present
CC invention
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RERK 8
 ||||
Db 8 RERK 11

RESULT 5

AAU96240

ID AAU96240 standard; peptide; 11 AA.

XX

AC AAU96240;

XX

DT 15-JUL-2002 (first entry)

XX

DE Class I G protein-coupled receptor #2.

XX

KW Class I G protein-coupled; receptor; mu opioid receptor;

KW altered signalling; basal activity; silencing mutation.

XX

OS Synthetic.

XX

PN WO200227015-A2.

XX

PD 04-APR-2002.

XX

PF 28-SEP-2001; 2001WO-US042416.

XX

PR 28-SEP-2000; 2000US-0236302P.

PR 03-MAY-2001; 2001US-0288644P.

XX

PA (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

XX

PI Kopin AS, Beinborn M;

XX

DR WPI; 2002-330100/36.

XX

PT Identifying polymorphic receptors having altered signaling, useful for
PT e.g. detecting receptors with alterations in their basal activity, such
PT as constitutively active receptors or receptors having silencing
PT mutations.

XX

PS Example 1; Fig 1; 7lpp; English.

XX

CC The invention relates to a method of identifying a polymorphic receptor
CC (e.g. a G-protein coupled receptor) having altered signalling, comprising
CC co-transfecting a host cell with a reporter construct and an expression
CC vector, in which the reporter construct comprises a response element and
CC a promoter operably linked to a reporter gene. The response element is
CC sensitive to a signal induced by the receptor and the expression vector
CC comprises a promoter operably linked to a candidate receptor containing a
CC genetic polymorphism. A second host cell is co-transfected with the
CC reporter construct and a negative control vector and the expression level
CC of the reporter construct in the host cells is measured. An increased or
CC decreased level of expression in the first host cell compared to the
CC second, identifies the candidate receptor as a polymorphic receptor with
CC altered signalling. The method is used for the identification of
CC receptors with alterations in their basal activity, for example,
CC constitutively active receptors or receptors having silencing mutations.

CC Other uses include the identification of polymorphic or mutant receptors
CC having alterations in signalling and receptors having altered drug
CC responses. The receptors identified are useful as tools for drug
CC discovery. Sequences AAU96239-AAU96313 represent Class I G protein-
CC coupled receptors, used in the identification of a constitutively active
CC rat mu opioid receptor

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RERK 8
| | | |
Db 1 RERK 4

RESULT 6

AAE34290

ID AAE34290 standard; peptide; 11 AA.

XX

AC AAE34290;

XX

DT 02-MAY-2003 (first entry)

XX

DE Human 5-hydroxytryptamine 1B receptor mutant peptide.

XX

KW Human; signalling; receptor; G protein-coupled receptor; GPCR; therapy;
KW 5-hydroxytryptamine; mutein; mutant.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 6

FT /note= "Wild type Thr substituted with Xaa; where Xaa =
FT Lys, Arg, Gln"

XX

PN WO200290926-A2.

XX

PD 14-NOV-2002.

XX

PF 03-MAY-2002; 2002WO-US014227.

XX

PR 03-MAY-2001; 2001US-0288647P.

XX

PA (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

XX

PI Kopin AS, Beinborn M;

XX

DR WPI; 2003-120567/11.

XX

PT Identifying receptor, e.g., G protein-coupled receptor, having
PT alterations in ligand dependent or independent signaling comprises
PT comparison of dose-response curves for expression of a reporter
PT construct.

XX
PS Disclosure; Page; 6lpp; English.
XX
CC The invention relates to a method of identifying receptor with altered
CC signalling. The method involves co-transfecting a cell with expression
CC vector having promoter linked to receptor and reporter construct having
CC response element and promoter linked to reporter gene, co-transfecting
CC another cell with reporter construct and negative control vector, and
CC measuring level of reporter construct at varying concentrations of
CC construct/vectors to give dose-response curves. The method is useful for
CC identifying a receptor that is a mutant receptor or polymorphic receptor
CC with altered signalling. The method is especially useful for identifying
CC a G protein-coupled receptor (GPCR) with altered signalling where the
CC GPCR is selected from a constitutively active receptor, hypersensitive
CC receptor, hyposensitive receptor, non-functional receptor, silent
CC receptor or partially silent receptor. Receptor with altered signalling
CC is useful in drug screening assays to identify ligands for treating a
CC disease or disorder. The present sequence is human 5-hydroxytryptamine 1B
CC receptor mutant peptide used in the invention. Note: This sequence is not
CC shown in the specification but is derived from the human 5-
CC hydroxytryptamine 1B receptor wild-type peptide shown in figure 9 of the
CC specification (AAE34216)
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RERK 8
| | | |
Db 1 RERK 4

RESULT 7
AAE34216
ID AAE34216 standard; peptide; 11 AA.
XX
AC AAE34216;
XX
DT 02-MAY-2003 (first entry)
XX
DE Human 5-hydroxytryptamine 1B receptor peptide.
XX
KW Human; signalling; receptor; G protein-coupled receptor; GPCR; therapy;
KW 5-hydroxytryptamine receptor.
XX
OS Homo sapiens.
XX
PN WO200290926-A2.
XX
PD 14-NOV-2002.
XX
PF 03-MAY-2002; 2002WO-US014227.
XX
PR 03-MAY-2001; 2001US-0288647P.
XX

PA (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

XX

PI Kopin AS, Beinborn M;

XX

DR WPI; 2003-120567/11.

XX

PT Identifying receptor, e.g., G protein-coupled receptor, having
PT alterations in ligand dependent or independent signaling comprises
PT comparison of dose-response curves for expression of a reporter
PT construct.

XX

PS Disclosure; Fig 9; 6lpp; English.

XX

CC The invention relates to a method of identifying receptor with altered
CC signalling. The method involves co-transfecting a cell with expression
CC vector having promoter linked to receptor and reporter construct having
CC response element and promoter linked to reporter gene, co-transfecting
CC another cell with reporter construct and negative control vector, and
CC measuring level of reporter construct at varying concentrations of
CC construct/vectors to give dose-response curves. The method is useful for
CC identifying a receptor that is a mutant receptor or polymorphic receptor
CC with altered signalling. The method is especially useful for identifying
CC a G protein-coupled receptor (GPCR) with altered signalling where the
CC GPCR is selected from a constitutively active receptor, hypersensitive
CC receptor, hyposensitive receptor, non-functional receptor, silent
CC receptor or partially silent receptor. Receptor with altered signalling
CC is useful in drug screening assays to identify ligands for treating a
CC disease or disorder. The present sequence is human 5-hydroxytryptamine 1B
CC receptor peptide used in the invention

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 6; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RERK 8

||||

Db 1 RERK 4

RESULT 8

AAP40439

ID AAP40439 standard; peptide; 11 AA.

XX

AC AAP40439;

XX

DT 25-MAR-2003 (revised)

DT 03-OCT-2002 (revised)

DT 14-FEB-1992 (first entry)

XX

DE Sequence of peptide with immunomodulating activity.

XX

KW Immunopotentiator; antimicrobial; antiviral; immunomodulator.

XX

OS Synthetic.

XX

PN EP103858-A.
 XX
 PD 28-MAR-1984.
 XX
 PF 16-SEP-1983; 83EP-00109147.
 XX
 PR 17-SEP-1982; 82JP-00162873.
 PR 25-NOV-1982; 82JP-00207335.
 XX
 PA (FUJI) FUJISAWA PHARM CO LTD.
 XX
 PI Hashimoto M, Hemmi K;
 XX
 DR WPI; 1984-083584/14.
 XX
 PT Penta- to tri-deca:peptide(s) - useful as strong immuno-potentiators esp.
 PT against microbes and viruses.
 XX
 PS Claim 1; Page 82; 87pp; English.
 XX
 CC The first AA of each claimed peptide is bonded to H and the final AA is
 CC bonded to OH. The peptides are useful as antimicrobial and antiviral
 CC agents. Dose is 0.1-1000 mg/kg. daily. (Updated on 03-OCT-2002 to add
 CC missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KSK 10
 |||
 Db 1 KSK 3

RESULT 9

AAP40131

ID AAP40131 standard; protein; 11 AA.

XX

AC AAP40131;

XX

DT 03-OCT-2002 (revised)

DT 12-FEB-1992 (first entry)

XX

DE Clones pJDB207/IF2(51) delta 72 at junction (Xho linker) between the
 DE 3'UTR of IFN-51 and the PHO5 transcription termination region.

XX

KW Yeast expression vector; promoter.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Protein 1. .11

FT /label= IFN-51

XX

PN EP100561-A.

XX
 PD 15-FEB-1984.
 XX
 PF 08-AUG-1983; 83EP-00107804.
 XX
 PR 09-AUG-1982; 82GB-00022883.
 PR 31-DEC-1982; 82GB-00037026.
 PR 02-JUN-1983; 83GB-00015145.
 PR 14-JUL-1983; 83GB-00019099.
 XX
 PA (CIBA) CIBA GEIGY AG.
 XX
 PI Hinnen A, Meyhack B, Meyer F;
 XX
 DR WPI; 1984-044243/08.
 DR N-PSDB; AAN40115.
 XX
 PT Acid phosphatase promoting DNA fragment - for expressing peptide(s) in
 PT yeasts which are more easily cultured than e.coli.
 XX
 PS Example; Fig 28a; 166pp; English.
 XX
 CC The inventors claim: (A) DNA fragment consisting of yeast acid
 CC phosphatase promoter and flanking sequences or its mutants which retain
 CC the promoter function. (B) Hybrid vector consisting of a yeast acid
 CC phosphatase promoter and a yeast or non-yeast polypeptide coding region
 CC controlled by the promoter. (C) A yeast transformed by the vector. (D)
 CC Prodn. of a yeast or non-yeast polypeptide or its deriv. by culturing the
 CC transformed yeast. The polypeptides are hormones, antiviral and
 CC anticancer peptides, enzymes and interferon. (Updated on 03-OCT-2002 to
 CC add missing OS field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KSK 10
 |||
 Db 8 KSK 10

RESULT 10 AAP40132

ID AAP40132 standard; protein; 11 AA.
 XX
 AC AAP40132;
 XX
 DT 03-OCT-2002 (revised)
 DT 12-FEB-1992 (first entry)
 XX
 DE Clones pJDB207/IF2(51) delta 82 at the junction (Xho linker) between the
 DE 3'UTR of IFN-51 and the PHO5 transcription termination region.
 XX
 KW Yeast expression vector; promoter.
 XX

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 1. .11
 FT /label= IFN-51
 XX
 PN EP100561-A.
 XX
 PD 15-FEB-1984.
 XX
 PF 08-AUG-1983; 83EP-00107804.
 XX
 PR 09-AUG-1982; 82GB-00022883.
 PR 31-DEC-1982; 82GB-00037026.
 PR 02-JUN-1983; 83GB-00015145.
 PR 14-JUL-1983; 83GB-00019099.
 XX
 PA (CIBA) CIBA GEIGY AG.
 XX
 PI Hinnen A, Meyhack B, Meyer F;
 XX
 DR WPI; 1984-044243/08.
 DR N-PSDB; AAN40116.
 XX
 PT Acid phosphatase promoting DNA fragment - for expressing peptide(s) in
 PT yeasts which are more easily cultured than e.coli.
 XX
 PS Example; Fig 28b; 166pp; English.
 XX
 CC The inventors claim: (A) DNA fragment consisting of yeast acid
 CC phosphatase promoter and flanking sequences or its mutants which retain
 CC the promoter function. (B) Hybrid vector consisting of a yeast acid
 CC phosphatase promoter and a yeast or non-yeast polypeptide coding region
 CC controlled by the promoter. (C) A yeast transformed by the vector. (D)
 CC Prodn. of a yeast or non-yeast polypeptide or its deriv. by culturing the
 CC transformed yeast. The polypeptides are hormones, antiviral and
 CC anticancer peptides, enzymes and interferon. (Updated on 03-OCT-2002 to
 CC add missing OS field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KSK 10
 |||
 Db 8 KSK 10

RESULT 11
 AAP60142
 ID AAP60142 standard; peptide; 11 AA.
 XX
 AC AAP60142;
 XX
 DT 25-MAR-2003 (revised)

DT 31-OCT-2002 (revised)
 DT 07-JUL-1991 (first entry)
 XX
 DE Type 3 pentapeptide linked to VP3 peptide suitable for use in a vaccine
 DE against a disease caused by type 3 poliovirus.
 XX
 KW Vaccine; diagnosis; enterovirus disease; poliovirus type 1; type 2;
 KW type 3.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1. .5
 FT /label= type 3 pentapeptide
 FT Misc-difference 1
 FT /label= R,K
 FT /note= "pref. R"
 FT Misc-difference 2
 FT /label= N,Q,D,E
 FT /note= "pref. N"
 FT Misc-difference 3
 FT /label= see above
 FT Misc-difference 5
 FT /label= D,E
 FT /note= "pref. D"
 FT Region 6. .11
 FT /label= VP3 peptide
 XX
 PN EP197772-A.
 XX
 PD 15-OCT-1986.
 XX
 PF 03-APR-1986; 86EP-00302481.
 XX
 PR 03-APR-1985; 85GB-00008685.
 PR 03-APR-1986; 86GB-00008140.
 XX
 PA (NATR) NAT RES DEV CORP.
 PA (BRTE-) BRITISH TECHNOLOGY GROUP LTD.
 XX
 PI Minor PD, Evans DMA, Schild GC, Almond JW, Ferguson M;
 XX
 DR WPI; 1986-273645/42.
 XX
 PT Synthetic peptide for vaccination or diagnosis of enter-virus disease -
 PT comprises fragment coded for by polio virus type 3 Sabin strain capsid
 PT protein RNA.
 XX
 PS Disclosure; Page 15; 53pp; English.
 XX
 CC The inventors claim synthetic peptides for use in vaccination against or
 CC diagnosis of a disease caused by an enterovirus (see AAN60118). The
 CC peptides are coded for by codons 286-288 or 286-290 in the RNA sequence
 CC coding for the structural capsid protein VP1 of poliovirus type 3 Sabin
 CC strain or by equivalent codons of another enterovirus, or antigenic
 CC equivs. Also claimed are synthetic peptides comprising the above peptides
 CC linked to (a) a hexapeptide coded for by codons 93-98 as above, or (b) a

CC peptide sequence comprising AA residues 58 and 59 of the VP3 capsid
CC protein of an enterovirus. Typical doses are 100mg-1mg, i.m. (Updated on
CC 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct
CC PA field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SKD 11
|||
Db 8 SKD 10

RESULT 12

AAP91264

ID AAP91264 standard; peptide; 11 AA.

XX

AC AAP91264;

XX

DT 25-MAR-2003 (revised)

DT 20-DEC-1989 (first entry)

XX

DE Tissue plasminogen activator mutant EGAV (V51R: N451Q).

XX

KW Tissue plasminogen activator; mutant; fibrinolysis; EGAV (V51R: N451Q).

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 7

XX

PN WO8907146-A.

XX

PD 10-AUG-1989.

XX

PF 03-FEB-1989; 89WO-US000465.

XX

PR 05-FEB-1988; 88US-00152692.

XX

PA (INTE-) INTEG GENETICS INC.

XX

PI Markland W, Livingston DJ;

XX

DR WPI; 1989-249015/34.

XX

PT Rearranged tissue plasminogen activators - prepd. by altering the DNA
PT sequence to introduce Avr II, Nhe I, Spe I or Xba I cleavage sites.

XX

PS Disclosure; Page 36; 77pp; English.

XX

CC The peptide is encoded by AAN90545. The peptide has tPA activity, with
CC extended in vivo half life. Spacing between tPA domains is increased, to
CC increase rate of fibrinolysis or the resistance to inhibition by
CC endogenous tPA inhibitors present in human plasma. The peptide is used

CC for thrombolysis in the treatment of myocardial infarction, pulmonary
CC embolism, deep vein thrombosis and stroke. See also AAP91265-84. (Updated
CC on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKS 9
| | |
Db 7 RKS 9

RESULT 13

AAR06754

ID AAR06754 standard; protein; 11 AA.

XX

AC AAR06754;

XX

DT 25-MAR-2003 (revised)

DT 23-OCT-1990 (first entry)

XX

DE Tumour necrosis factor derived peptide.

XX

KW Tumour necrosis factor; TNF; neoplastic disease; autoimmune disease;
KW infection; inflammation; transplant rejection.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 5. .5

FT /label= K, Q, R

XX

PN DE3841753-A.

XX

PD 13-JUN-1990.

XX

PF 12-DEC-1988; 88DE-03841753.

XX

PR 12-DEC-1988; 88DE-03841753.

XX

PA (BADI) BASF AG.

PA (BOEH/) BOEHRM H J.

XX

PI Bohm HJ, Daum L, Schmied B, Walker N, Zechel JC, Haupt A;

XX

DR WPI; 1990-186573/25.

XX

PT New tumour necrosis factor derived peptide(s) - for treating or
PT preventing neoplastic and auto-immune disease, infection, inflammation
PT and transplant rejection.

XX

PS Example 67; Page 11; 15pp; German.

XX

CC To residue F1 is attached Ac and to residue A11 NH2. A3 and K9 form

CC together a covalent bond. This peptide is an example of a highly generic
 CC sequence of the formula X-A-G-D-Y. A= K,Q or R; X= G-NH-CHM-CO, G-NH-CHM-
 CC CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W; Y= Z, NH-CHQ-COZ, V-NH-CHQ-COZ,
 CC NH-CHQ-CO-U-Z or V-NH-CHQ-CO-U-Z; G= H or an amino protecting group; Z=
 CC OH, NH2 or carboxy protecting group; or G and Z together are a covalent
 CC bond or the gp. CO(CH2)aNH; a=1-12; R,U,V and W= peptide chains of 1-4
 CC naturally occurring alpha aminoacids; M and Q= H, isopropyl, CHMe.Et,
 CC phenyl, CH(OH).Me, 3-indolyl- or 4-imidazolyl-methyl or (CH2)bT; b=1-6; T=
 CC OH, MeO, MeS, Me2CH, phenyl (opt. 4-OH, substd), HS, NH2, COOH, CONH2, NH
 CC C (NH) NH2; or M and Q together are (CH2)c-S-S-(CH2)d, (CH2)eCO NH-(CH2)f
 CC or (CH2)eNH CO(CH2)gNH CO(CH2) f; c and d=1-4; e and f=1-6; g=1-12. The
 CC peptide is a low mol. wt. deriv. of TNF. See also DE3841753-55,
 CC DE3841759, DE3841761-64, DE3841767-68. (Updated on 25-MAR-2003 to correct
 CC PA field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKS 9
 |||
 Db 8 RKS 10

RESULT 14

AAR10931

ID AAR10931 standard; peptide; 11 AA.

XX

AC AAR10931;

XX

DT 07-MAY-1991 (first entry)

XX

DE Relaxin C peptide epitope IV.

XX

KW Monoclonal antibody; pregnancy; antigen; immunogen.

XX

OS Synthetic.

XX

PN WO9102251-A.

XX

PD 21-FEB-1991.

XX

PF 07-AUG-1989; 89US-00390626.

XX

PR 07-AUG-1989; 89US-00390626.

XX

PA (ITCA-) INT CANINE GENETICS.

XX

PI Kuniyuki AH;

XX

DR WPI; 1991-073676/10.

XX

PT Detection of pregnancy in animals, esp. cats and dogs - by identifying
 PT the presence of the C peptide of relaxin in body fluids.

XX

PS Claim 19; Page 38; 42pp; English.

XX

CC The peptide corresponds to residues 94-104 of rat relaxin C peptide. The
CC peptide was used as an immunogen to generate monoclonal anti- bodies for
CC use in detecting pregnancy. See also AAR10928-R10930

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ERK 8

|||

Db 5 ERK 7

RESULT 15

AAR12375

ID AAR12375 standard; protein; 11 AA.

XX

AC AAR12375;

XX

DT 25-MAR-2003 (revised)

DT 15-AUG-1991 (first entry)

XX

DE Human Factor VII (330-340) antihemostatic peptide.

XX

KW anti-coagulant; thrombosis; Factor VII-tissue factor complex.

XX

OS Synthetic.

XX

PN WO9107432-A.

XX

PD 30-MAY-1991.

XX

PF 13-NOV-1989; 89US-00435657.

XX

PR 13-NOV-1989; 89US-00435657.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX

PI Fair DS, Kumar A;

XX

DR WPI; 1991-178057/24.

XX

PT New anti-hemostatic oligo peptide(s) - inhibit rate of extrinsic pathway
PT mediated activation-formation of Factor X or rate of thrombin formation.

XX

PS Claim 21; Page 41; 62pp; English.

XX

CC Compositions comprising this peptide or peptides having at least 95 per
CC cent homology to a sequence of 10-15 amino acids selected from it, are
CC useful for treatment of clotting or thrombotic disorders. The peptide is
CC disclosed as new and inhibits Factor Xa formation by about 40 per cent.
CC See also AAR12370-4, AAR12376-7 and AAR13010-R13011. (Updated on 25-MAR-
CC 2003 to correct PA field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SKD 11

|||

Db 7 SKD 9

RESULT 16

AAR22743

ID AAR22743 standard; protein; 11 AA.

XX

AC AAR22743;

XX

DT 25-MAR-2003 (revised)

DT 27-AUG-1992 (first entry)

XX

DE Non-A, Non-B hepatitis virus antibody binding peptide.

XX

KW NANBH; immunoreactive; detection.

XX

OS Synthetic.

XX

PN EP479376-A.

XX

PD 08-APR-1992.

XX

PF 05-OCT-1990; 90EP-00202658.

XX

PR 26-SEP-1991; 91EP-00202498.

XX

PA (ALKU) AKZO NV.

XX

PI Habets WJA;

XX

DR WPI; 1992-116131/15.

XX

PT New peptide(s) reactive with antibodies to hepatitis non-A, non-B, virus
PT - for detection of NANBH and its antibodies in body fluids.

XX

PS Example; Page 7; 9pp; English.

XX

CC The sequence is that of a peptide which is immunoreactive with antibodies
CC to hepatitis non-A, non-B (NANBH) virus, it was prepd. by stepwise solid
CC phase peptide synthesis. It can be used to detect NANBH antibodies in
CC test fluids. It has improved immunochemical reactivity, a high affinity
CC to NANBH antibodies and is of a safe, non-infectious origin. See also
CC AAR22727-R22744. (Updated on 25-MAR-2003 to correct PF field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKT 4
|||
Db 2 RKT 4

RESULT 17

AAR31357

ID AAR31357 standard; peptide; 11 AA.

XX

AC AAR31357;

XX

DT 25-MAR-2003 (revised)

DT 20-MAY-1998 (first entry)

XX

DE Antimicrobial peptide #11 derived from bovine lactoferrin.

XX

KW antimicrobial agent; iron-binding protein; athlete's foot; mastitis;

KW antibacterial agent.

XX

OS Synthetic.

XX

PN EP503939-A1.

XX

PD 16-SEP-1992.

XX

PF 12-MAR-1992; 92EP-00302125.

XX

PR 13-MAR-1991; 91JP-00048196.

PR 24-APR-1991; 91JP-00094492.

PR 24-APR-1991; 91JP-00094493.

XX

PA (MORG) MORINAGA MILK IND CO LTD.

XX

PI Tomita M, Kawase K, Takase M, Bellamy WR, Yamauchi K;

PI Wakabayashi H, Tokita Y;

XX

DR WPI; 1992-310006/38.

XX

PT New antimicrobial peptide(s) - active against e.g. *Listeria*

PT *monocytogenes*, *Staphylococcus aureus*, *Pseudomonas aeruginosa* and

PT *Klebsiella pneumoniae*, for treating e.g. diarrhoea, mastitis, etc.

XX

PS Claim 8; Page 17; 19pp; English.

XX

CC This synthetic peptide has a sequence derived from bovine lactoferrin.

CC The peptide has stronger antimicrobial activity than unhydrolysed

CC lactoferrin and improved heat resistance. The peptide had a minimum

CC inhibitory concentration (microM) of 1.5, 3, 6 and 25 against *Listeria*

CC *monocytogenes*, *Staphylococcus aureus*, *Pseudomonas aeruginosa* and

CC *Klebsiella pneumoniae*, respectively. This and other peptides derived from

CC hydrolysed lactoferrin can be incorporated into foods, human or

CC veterinary compositions (e.g. for treating mastitis and athlete's foot),

CC toiletries, cosmetics, cleaning agents, etc. See AAR31350-R31361.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KTR 5
|||
Db 1 KTR 3

RESULT 18

AAR28089

ID AAR28089 standard; protein; 11 AA.

XX

AC AAR28089;

XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)

XX

DE Cell-to-cell binding inhibiting peptide subunit (14).

XX

KW Adhesion; integrin; multimer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cross-links 5. .11

FT /note= "sequence linked by interchain amide bond at Glu
FT position to Lys residue on Arg4-Lys-Arg-Ser-Arg-Gly-Asp-
FT Val sequence (see AAR28090)"

XX

PN WO9208476-A1.

XX

PD 29-MAY-1992.

XX

PF 07-NOV-1991; 91WO-US008328.

XX

PR 07-NOV-1990; 90US-00610363.

XX

PA (SCRI) SCRIPPS RES INST.

XX

PI Ruggeri ZM, Houghten RA;

XX

DR WPI; 1992-199940/24.

XX

PT Peptides inhibiting binding of adhesion mols. to cells expressing
PT integrins - for treating and preventing thrombus formation and diseases
PT associated with platelet aggregation.

XX

PS Disclosure; Page 39-40; 70pp; English.

XX

CC A peptide which inhibits binding of adhesion mols. to cells expressing
CC integrins comprises two subunits having the sequences given in AAR28089-
CC 90, held together by an interchain stable bond. The sequence RGD is in
CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RER 7
|||
Db 4 RER 6

RESULT 19

AAR28088

ID AAR28088 standard; protein; 11 AA.

XX

AC AAR28088;

XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)

XX

DE Cell-to-cell binding inhibiting peptide subunit (13).

XX

KW Adhesion; integrin; multimer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cross-links 6. .11

FT /note= "sequence linked by interchain amide bond at Lys
FT position to Glu residue on Arg5-Glu-Ser-Arg-Gly-Asp-Val
FT sequence (see AAR28087)"

XX

PN WO9208476-A1.

XX

PD 29-MAY-1992.

XX

PF 07-NOV-1991; 91WO-US008328.

XX

PR 07-NOV-1990; 90US-00610363.

XX

PA (SCRI) SCRIPPS RES INST.

XX

PI Ruggeri ZM, Houghten RA;

XX

DR WPI; 1992-199940/24.

XX

PT Peptides inhibiting binding of adhesion mols. to cells expressing
PT integrins - for treating and preventing thrombus formation and diseases
PT associated with platelet aggregation.

XX

PS Disclosure; Page 37-38; 70pp; English.

XX

CC A peptide which inhibits binding of adhesion mols. to cells expressing
CC integrins comprises two subunits having the sequences given in AAR28087-
CC 88, held together by an interchain stable bond. The sequence RGD is in
CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKS 9
|||
Db 5 RKS 7

RESULT 20

AAR28128

ID AAR28128 standard; protein; 11 AA.

XX

AC AAR28128;

XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)

XX

DE Cell-to-cell binding inhibiting peptide subunit (16).

XX

KW Adhesion; integrin; multimer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cross-links 4. .11

FT /note= "sequence linked by interchain amide bond at Glu

FT position to Lys residue on Arg3-Lys-Arg2-Ser-Arg-Gly-Asp-

FT Val sequence (see AAR28129)"

XX

PN WO9208476-A1.

XX

PD 29-MAY-1992.

XX

PF 07-NOV-1991; 91WO-US008328.

XX

PR 07-NOV-1990; 90US-00610363.

XX

PA (SCRI) SCRIPPS RES INST.

XX

PI Ruggeri ZM, Houghten RA;

XX

DR WPI; 1992-199940/24.

XX

PT Peptides inhibiting binding of adhesion mols. to cells expressing
PT integrins - for treating and preventing thrombus formation and diseases
PT associated with platelet aggregation.

XX

PS Disclosure; Page 40-41; 70pp; English.

XX

CC A peptide which inhibits binding of adhesion mols. to cells expressing
CC integrins comprises two subunits having the sequences given in AAR28128-
CC 29, held together by an interchain stable bond. The sequence RGD is in
CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RER 7
|||
Db 3 RER 5

RESULT 21

AAR28130

ID AAR28130 standard; protein; 11 AA.

XX

AC AAR28130;

XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)

XX

DE Cell-to-cell binding inhibiting peptide subunit (18).

XX

KW Adhesion; integrin; multimer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cross-links 3. .11

FT /note= "sequence linked by interchain amide bond at Glu
FT position to Lys residue on Arg2-Lys-Arg3-Ser-Arg-Gly-Asp-
FT Val sequence (see AAR28131)"

XX

PN WO9208476-A1.

XX

PD 29-MAY-1992.

XX

PF 07-NOV-1991; 91WO-US008328.

XX

PR 07-NOV-1990; 90US-00610363.

XX

PA (SCRI) SCRIPPS RES INST.

XX

PI Ruggeri ZM, Houghten RA;

XX

DR WPI; 1992-199940/24.

XX

PT Peptides inhibiting binding of adhesion mols. to cells expressing
PT integrins - for treating and preventing thrombus formation and diseases
PT associated with platelet aggregation.

XX

PS Disclosure; Page 41-43; 70pp; English.

XX

CC A peptide which inhibits binding of adhesion mols. to cells expressing
CC integrins comprises two subunits having the sequences given in AAR28130-
CC 31, held together by an interchain stable bond. The sequence RGD is in
CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RER 7

|||

Db 2 RER 4

RESULT 22

AAR28132

ID AAR28132 standard; protein; 11 AA.

XX

AC AAR28132;

XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)

XX

DE Cell-to-cell binding inhibiting peptide subunit (20).

XX

KW Adhesion; integrin; multimer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cross-links 2. .11

FT /note= "sequence linked by interchain amide bond at Glu

FT position to Lys residue on Arg-Lys-Arg4-Ser-Arg-Gly-Asp-

FT Val sequence (see AAR28133)"

XX

PN W09208476-A1.

XX

PD 29-MAY-1992.

XX

PF 07-NOV-1991; 91WO-US008328.

XX

PR 07-NOV-1990; 90US-00610363.

XX

PA (SCRI) SCRIPPS RES INST.

XX

PI Ruggeri ZM, Houghten RA;

XX

DR WPI; 1992-199940/24.

XX

PT Peptides inhibiting binding of adhesion mols. to cells expressing

PT integrins - for treating and preventing thrombus formation and diseases

PT associated with platelet aggregation.

XX

PS Disclosure; Page 43-44; 70pp; English.

XX

CC A peptide which inhibits binding of adhesion mols. to cells expressing

CC integrins comprises two subunits having the sequences given in AAR28132-

CC 33, held together by an interchain stable bond. The sequence RGD is in

CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RER 7
|||
Db 1 RER 3

RESULT 23

AAR44843

ID AAR44843 standard; peptide; 11 AA.

XX

AC AAR44843;

XX

DT 25-MAR-2003 (revised)

DT 09-JAN-2003 (revised)

DT 31-JAN-1994 (first entry)

XX

DE Lactoferrin-related antibacterial peptide.

XX

KW Lactoferrin; antibiotic; chelate; mastitis; bowel disorder; disease;

KW bacteria; yeast; fungi; disinfection; drug; foodstuff; cosmetic;

KW toiletries.

XX

OS Unidentified.

XX

PN WO9314640-A1.

XX

PD 05-AUG-1993.

XX

PF 30-NOV-1992; 92WO-JP001563.

XX

PR 23-JAN-1992; 92JP-00032660.

PR 11-MAR-1992; 92JP-00052943.

PR 30-SEP-1992; 92JP-00262143.

PR 30-SEP-1992; 92JP-00262559.

XX

PA (MORG) MORINAGA MILK IND CO LTD.

XX

PI Tomita M, Shimamura S, Kawase K, Fukuwatari Y, Takase M;

PI Bellamy W, Yamauchi K, Wakabayashi H, Tokita Y;

XX

DR WPI; 1993-258265/32.

XX

PT Antibacterial agent comprising decomposition products of lactoferrin -

PT with chelate e.g. EDTA alcohol and/or antibiotic e.g. penicillin, also

PT useful against yeast and fungi.

XX

PS Disclosure; Page 86; 100pp; Japanese.

XX

CC Lactoferrin-related peptides are used in new antibacterial compsn. The

CC compsn. is highly effective against a broad range of bacteria, yeasts and

CC fungi. It can be used therapeutically (internal and external

CC application), e.g. for mastitis, bowel disorders, urinary infections,

CC etc. It can also be used for the disinfection and protection of drugs,
CC foodstuffs, cosmetics and toiletries and household items (such as kitchen
CC towels and toilet paper). (Updated on 09-JAN-2003 to add missing OS
CC field.) (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KTR 5
|||
Db 1 KTR 3

RESULT 24

AAR32352

ID AAR32352 standard; peptide; 11 AA.

XX

AC AAR32352;

XX

DT 05-JUL-1993 (first entry)

XX

DE Human Factor X peptide.

XX

KW Anticoagulant; intrinsic; extrinsic; prothrombin activation; thrombin;
KW formation; Factor Xa; pathway mediated activation; inhibition.

XX

OS Synthetic.

XX

PN US5187155-A.

XX

PD 16-FEB-1993.

XX

PF 23-JUN-1989; 89US-00371561.

XX

PR 23-JUN-1989; 89US-00371561.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX

PI Fair DS;

XX

DR WPI; 1993-075751/09.

XX

PT Compsns. comprising peptide(s) of 10-50 aminoacid residues - inhibit
PT factor X activation and/or Factor Xa function, useful for preventing
PT blood clot formation and treating deep vein thrombosis, pulmonary
PT embolism, etc.

XX

PS Example; Page 6; 23pp; English.

XX

CC The sequence is that of a peptide corresponding to amino acids 404-414 of
CC the human factor X molecule which was tested for its effect, (as a % of
CC the control rate), on the rate of Factor Xa formation and on the rate of
CC thrombin formation. The results obt'd. were for activation of Factor X by
CC the extrinsic activation complex 78%, by the intrinsic activation complex

CC 98%, and activation by RVV-X, 76%. For the rate of thrombin formation the
CC rate was 88% as compared to the control rate
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 1 ARK 3

RESULT 25

AAR37430

ID AAR37430 standard; peptide; 11 AA.

XX

AC AAR37430;

XX

DT 25-MAR-2003 (revised)

DT 08-SEP-1993 (first entry)

XX

DE Promega peptide 5.

XX

KW Modified peptide substrate; non-radioactive; detection; dansyl;
KW sulphorhodamine 101; lissamine; rhodamine; enzymes; phosphatases;
KW protein kinases; proteases.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "detection tag= lissamine, Rhodamine"

XX

PN W09310461-A1.

XX

PD 27-MAY-1993.

XX

PF 12-NOV-1992; 92WO-US009595.

XX

PR 12-NOV-1991; 91US-00791928.

XX

PA (PROM-) PROMEGA CORP.

XX

PI Shultz JW, White DH;

XX

DR WPI; 1993-182698/22.

XX

PT Quantitating presence or activity of enzyme - by incubating with modified
PT peptide substrate and measuring the modified peptide prod.

XX

PS Claim 24; Page 27; 103pp; English.

XX

CC Promega peptide 5 is tagged with dansyl at residue 1 and may be used in a
CC novel non-radioactive method of quantitating the presence or activity of
CC an enzyme. The method can be used for rapid, specific and highly

CC sensitive detection of enzymes such as protein kinases, phosphatases and
CC proteases, esp. in this case protein kinase C. They can be used to study
CC enzyme function in metabolism and in diagnosis of disease. They also
CC allow quantitative determ. of the enzyme's activity. See also AAR37426-
CC 36. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKS 9

|||

Db 5 RKS 7

RESULT 26

AAR34421

ID AAR34421 standard; peptide; 11 AA.

XX

AC AAR34421;

XX

DT 25-MAR-2003 (revised)

DT 05-AUG-1993 (first entry)

XX

DE Hepatitis C Ab detection peptide #5.

XX

KW Test reagent; detection; antibody; hepatitis C; virus; HCV; epitope;
KW structural region; diagnosis; ss.

XX

OS Synthetic.

XX

PN WO9307488-A1.

XX

PD 15-APR-1993.

XX

PF 02-OCT-1992; 92WO-JP001276.

XX

PR 02-OCT-1991; 91JP-00255524.

PR 26-MAR-1992; 92JP-00068695.

XX

PA (EIKE) EIKEN KAGAKU KK.

PA (OSAU) UNIV OSAKA.

PA (TANA) TANABE SEIYAKU CO.

XX

PI Ishibashi K, Ito M, Yoshida I, Takamizawa A, Shibatani T;

XX

DR WPI; 1993-134624/16.

XX

PT Reagent for detecting antibodies to hepatitis C virus - comprises
PT peptide(s) with the same sequence as an epitope of an HCV structural
PT region.

XX

PS Disclosure; Page 43; 51pp; Japanese.

XX

CC The sequences given in AAR34417-25 are peptides which can be used in a

CC test reagent for the detection of antibodies against hepatitis C. The
CC peptides represent epitopes of an HCV structural region and they react
CC specifically with antibodies against the HCV structural region. Detection
CC is sensitive and accurate and allows diagnosis of the infection at a
CC very early stage. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKT 4
|||
Db 2 RKT 4

RESULT 27

AAR57464

ID AAR57464 standard; protein; 11 AA.

XX

AC AAR57464;

XX

DT 28-FEB-1995 (first entry)

XX

DE Lactoferrin derived peptide #27.

XX

KW Lactoferrin; chemical; enzymatic; hydrolysis; antimicrobial; antiseptic;
KW ischaemic disease.

XX

OS Mus musculus.

XX

PN JP06172200-A.

XX

PD 21-JUN-1994.

XX

PF 08-DEC-1992; 92JP-00327738.

XX

PR 08-DEC-1992; 92JP-00327738.

XX

PA (MORG) MORINAGA MILK IND CO LTD.

XX

DR WPI; 1994-238662/29.

XX

PT Brain protectant for preventing ischaemic diseases without side effects -
PT comprising 31 specified peptide(s), prepd. by lactoferrin hydrolysis.

XX

PS Disclosure; Page 10; 11pp; Japanese.

XX

CC The sequences given in AAR57438-68 represent fragments of lactoferrin
CC which were derived from the full length protein by chemical or enzyme
CC hydrolysis. These peptides have brain protecting properties, as well as
CC anti-microbial activity. Compositions containing these peptides may be
CC prepared with out the addition of antiseptics, and may be administered at
CC doses of at least 10 mg for parenteral administration and 100 mg for oral
CC administration. These peptides are stable, heat resistant, water soluble
CC and may be used for the prevention of ischaemic diseases without side

CC effects
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KTR 5
|||
Db 1 KTR 3

RESULT 28

AAR66080

ID AAR66080 standard; peptide; 11 AA.

XX

AC AAR66080;

XX

DT 25-MAR-2003 (revised)

DT 18-JUL-1995 (first entry)

XX

DE Phosphorylated dbl peptide.

XX

KW Breast cancer; tumour specific antigen; phosphorylated dbl; antigen;

KW humoral; squamous cell carcinoma; SCC; peptide library; assay; detection;

KW diagnosis; vaccine; epitope.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 5

FT /note= "phosphorylated Tyr"

XX

PN WO9423728-A1.

XX

PD 27-OCT-1994.

XX

PF 12-APR-1994; 94WO-US003969.

XX

PR 16-APR-1993; 93US-00049698.

PR 03-FEB-1994; 94US-00191338.

XX

PA (NOUN) UNIV NORTHWESTERN.

XX

PI Calenoff E;

XX

DR WPI; 1994-341472/42.

XX

PT Identification 9 immunogenic cancer proteins - e.g. phosphorylated dbl

PT useful as peptide library of breast cancer specific humoral antigens.

XX

PS Claim 32; Page 86; 109pp; English.

XX

CC The invention relates to the identification and isolation of tumour-

CC specific antigens which can be used for early and specific detection of

CC tumours, for generating effector T-cells for adoptive immunotherapy, or

CC for formulating specific vaccines for individual tumour patients. Two
CC particular sets of antigens are described, one specific for squamous cell
CC carcinoma (SCC) and the other specific for breast cancer. Amongst the
CC antigens specific for breast cancer is found dbl protein which is
CC phosphorylated on at least one Ser, Thr or Tyr site. Phosphorylated p66
CC dbl protein for use as the antigen is described in AAR66067. The present
CC sequence is a phosphorylated antigenic peptide from dbl protein which is
CC also specific for breast cancer. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SKD 11
|||
Db 6 SKD 8

RESULT 29

AAR66072

ID AAR66072 standard; peptide; 11 AA.

XX

AC AAR66072;

XX

DT 25-MAR-2003 (revised)

DT 18-JUL-1995 (first entry)

XX

DE Phosphorylated dbl peptide.

XX

KW Breast cancer; tumour specific antigen; phosphorylated dbl; antigen;

KW humoral; squamous cell carcinoma; SCC; peptide library; assay; detection;

KW diagnosis; vaccine; epitope.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 6

FT /note= "phosphorylated Ser"

XX

PN WO9423728-A1.

XX

PD 27-OCT-1994.

XX

PF 12-APR-1994; 94WO-US003969.

XX

PR 16-APR-1993; 93US-00049698.

PR 03-FEB-1994; 94US-00191338.

XX

PA (NOUN) UNIV NORTHWESTERN.

XX

PI Calenoff E;

XX

DR WPI; 1994-341472/42.

XX

PT Identification 9 immunogenic cancer proteins - e.g. phosphorylated dbl
PT useful as peptide library of breast cancer specific humoral antigens.
XX
PS Claim 32; Page 86; 109pp; English.
XX
CC The invention relates to the identification and isolation of tumour-
CC specific antigens which can be used for early and specific detection of
CC tumours, for generating effector T-cells for adoptive immunotherapy, or
CC for formulating specific vaccines for individual tumour patients. Two
CC particular sets of antigens are described, one specific for squamous cell
CC carcinoma (SCC) and the other specific for breast cancer. Amongst the
CC antigens specific for breast cancer is found dbl protein which is
CC phosphorylated on at least one Ser, Thr or Tyr site. Phosphorylated p66
CC dbl protein for use as the antigen is described in AAR66067. The present
CC sequence is a phosphorylated antigenic peptide from dbl protein which is
CC also specific for breast cancer. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SKD 11
|||
Db 6 SKD 8

RESULT 30

AAR66083

ID AAR66083 standard; peptide; 11 AA.

XX

AC AAR66083;

XX

DT 25-MAR-2003 (revised)

DT 18-JUL-1995 (first entry)

XX

DE Phosphorylated dbl peptide.

XX

KW Breast cancer; tumour specific antigen; phosphorylated dbl; antigen;
KW humoral; squamous cell carcinoma; SCC; peptide library; assay; detection;
KW diagnosis; vaccine; epitope.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 5

FT /note= "phosphorylated Thr"

FT Modified-site 6

FT /note= "phosphorylated Ser"

XX

PN WO9423728-A1.

XX

PD 27-OCT-1994.

XX

PF 12-APR-1994; 94WO-US003969.

XX
 PR 16-APR-1993; 93US-00049698.
 PR 03-FEB-1994; 94US-00191338.
 XX
 PA (NOUN) UNIV NORTHWESTERN.
 XX
 PI Calenoff E;
 XX
 DR WPI; 1994-341472/42.
 XX
 PT Identification 9 immunogenic cancer proteins - e.g. phosphorylated dbl
 PT useful as peptide library of breast cancer specific humoral antigens.
 XX
 PS Claim 32; Page 86; 109pp; English.
 XX
 CC The invention relates to the identification and isolation of tumour-
 CC specific antigens which can be used for early and specific detection of
 CC tumours, for generating effector T-cells for adoptive immunotherapy, or
 CC for formulating specific vaccines for individual tumour patients. Two
 CC particular sets of antigens are described, one specific for squamous cell
 CC carcinoma (SCC) and the other specific for breast cancer. Amongst the
 CC antigens specific for breast cancer is found dbl protein which is
 CC phosphorylated on at least one Ser, Thr or Tyr site. Phosphorylated p66
 CC dbl protein for use as the antigen is described in AAR66067. The present
 CC sequence is a phosphorylated antigenic peptide from dbl protein which is
 CC also specific for breast cancer. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SKD 11
 |||
 Db 6 SKD 8

RESULT 31

AAR48537

ID AAR48537 standard; peptide; 11 AA.

XX

AC AAR48537;

XX

DT 25-MAR-2003 (revised)

DT 10-AUG-1994 (first entry)

XX

DE Lactoferrin derived peptide #31.

XX

KW Decomposition; lactoferrin; digestion; enzyme; pepsin; trypsin;
 KW antioxidant; oxidation; inhibitor; vitamin E; ascorbic acid; vitamin A;
 KW beta-carotene; superoxidase dismutase; coenzyme Q; lipid oxidation;
 KW foodstuff; drugs; health food; toiletries; cosmetics.

XX

OS Bos taurus.

XX

PN WO9403555-A1.
 XX
 PD 17-FEB-1994.
 XX
 PF 04-AUG-1993; 93WO-JP001090.
 XX
 PR 07-AUG-1992; 92JP-00211335.
 XX
 PA (MORG) MORINAGA MILK IND CO LTD.
 XX
 PI Tomita M, Shimamura S, Kawase K, Fukuwatari Y, Takase M;
 PI Bellamy WR, Yamauchi K, Wakabayashi H, Tokida Y;
 XX
 DR WPI; 1994-065650/08.
 XX
 PT Antioxidant peptide lactoferrin decomposition product - prevents
 PT oxidation of lipid(s) in foodstuffs and drugs without affecting their
 PT taste.
 XX
 PS Claim 3; Page 41; 47pp; Japanese.
 XX
 CC The sequences given in AAR48507-37 are peptides derived by the
 CC decomposition of lactoferrin, pref. by digestion with an enzyme, eg.
 CC pepsin or trypsin. These peptides may be used in an antioxidant
 CC composition which may also contain an oxidation inhibitor such as vitamin
 CC E, ascorbic acid, vitamin A, beta-carotene, superoxidase dismutase or
 CC coenzyme Q. The antioxidant prevents lipid oxidation in foodstuffs,
 CC drugs, health foods, toiletries and cosmetics. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KTR 5
 |||
 Db 1 KTR 3

RESULT 32

AAR63547

ID AAR63547 standard; peptide; 11 AA.

XX

AC AAR63547;

XX

DT 25-MAR-2003 (revised)

DT 07-JUN-1995 (first entry)

XX

DE HT-LCF peptide fragment from HPLC peak A.

XX

KW rHT-LCF; HT-1376 cell derived leukocyte chemotactic factor;

KW immunopotentiator; monocyte and macrophage migration factor;

KW wound healing.

XX

OS Homo sapiens.

XX
 PN WO9421809-A1.
 XX
 PD 29-SEP-1994.
 XX
 PF 11-MAR-1994; 94WO-JP000397.
 XX
 PR 15-MAR-1993; 93JP-00054349.
 XX
 PA (CYTO-) INST CYTOSIGNAL RES INC.
 XX
 PI Kawamura K, Watanabe K;
 XX
 DR WPI; 1994-317029/39.
 XX
 PT Monocyte and macrophage migration factor protein - is immuno-potentiator
 PT and vulnerary and is isolated from culture of HT-1376 cell line by
 PT recombinant methods.
 XX
 PS Example 16; Page 47; 68pp; Japanese.
 XX
 CC Proteins having monocyte and macrophage migration factor activity were
 CC isolated from human HT-1376 cells (ATCC CRL-1472). The proteins are
 CC useful as immunopotentiators for treatment of infections, immune
 CC deficiency diseases and cancer. The proteins are also useful in wound
 CC healing preparations and for treatment of skin diseases. AAR63547-R63551
 CC are peptide fragments isolated from different peaks observed following
 CC HPLC separation as part of the rHT-LCF isolation procedure. (Updated on
 CC 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KTR 5
 |||
 Db 7 KTR 9

RESULT 33
 AAR66534
 ID AAR66534 standard; peptide; 11 AA.
 XX
 AC AAR66534;
 XX
 DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 10-AUG-1995 (first entry)
 XX
 DE Human influenza virus M protein residues 41-51.
 XX
 KW Human major histocompatibility complex class I; MHC class I;
 KW allele HLA-A2.1; influenza M protein; matrix; membrane;
 KW HLA class I-restricted CD8+ cytotoxic T cell response.
 XX

OS Influenza virus.
 XX
 PN WO9426903-A2.
 XX
 PD 24-NOV-1994.
 XX
 PF 18-MAY-1994; 94WO-NL000114.
 XX
 PR 18-MAY-1993; 93EP-00201429.
 XX
 PA (UYLE-) RIJKSUNIV LEIDEN.
 PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
 XX
 PI Melief CJM, Kast WM;
 XX
 DR WPI; 1995-022282/03.
 XX
 PT Human influenza virus peptide(s) - have ability to bind Major
 PT Histocompatibility Complex Class I molecule, useful for treating
 PT influenza-related disease.
 XX
 PS Claim 4; Page 29; 33pp; English.
 XX
 CC Peptide sequences AAR66530-R66544 are derived from human influenza virus
 CC M protein and have the ability to bind to human MHC class I allele HLA-
 CC A2.1. The peptides are useful for inducing a T-cell response
 CC (specifically, an HLA class I-restricted CD8+ cytotoxic T cell response)
 CC effective against human influenza virus. (Updated on 25-MAR-2003 to
 CC correct PN field.) (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KTR 5
 |||
 Db 7 KTR 9

RESULT 34

AAR70606

ID AAR70606 standard; peptide; 11 AA.

XX

AC AAR70606;

XX

DT 14-FEB-1996 (first entry)

XX

DE HIV(B35)ARV2-7, human immunodeficiency virus epitope.

XX

KW HLA; human lymphocyte antigen; HIV; human immunodeficiency virus;

KW binding peptide; induce killer cell; prevention; treatment; AIDS;

KW autoimmune disease syndrome; vaccine.

XX

OS Human immunodeficiency virus.

XX

PN WO9511255-A1.
 XX
 PD 27-APR-1995.
 XX
 PF 19-OCT-1994; 94WO-JP001756.
 XX
 PR 19-OCT-1993; 93JP-00261302.
 XX
 PA (AJIN) AJINOMOTO KK.
 XX
 PI Takiguchi M, Miwa K;
 XX
 DR WPI; 1995-170188/22.
 XX
 PT HLA-binding peptide fragments from HIV proteins - induce killer cells
 PT which target HIV-infected cells and can be incorporated into anti-HIV
 PT vaccines.
 XX
 PS Example 1; Page 10; 6lpp; Japanese.
 XX
 CC AAR70606 is a peptide fragment derived from an HIV (Human
 CC Immunodeficiency Virus) protein and is capable of binding to a human
 CC lymphocyte antigen. The peptide can induce killer cells which target HIV-
 CC infected cells. It is also useful in the prevention and treatment of HIV
 CC and AIDS. Anti-HIV vaccines may incorporate the peptides, or may
 CC incorporate a vector (such as vaccinia or BCG) contg. DNA encoding the
 CC peptides
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKS 9
 |||
 Db 7 RKS 9

RESULT 35

AAR84701

ID AAR84701 standard; peptide; 11 AA.

XX

AC AAR84701;

XX

DT 13-JUN-1996 (first entry)

XX

DE Bovine lactoferrin derived angina pectoris treating peptide.

XX

KW Bovine lactoferrin; angina pectoris; treatment; low toxicity;
 KW no side effects; heat resistance; water solubility; stability;
 KW aqueous solution; preservative free.

XX

OS Bos taurus.

XX

PN JP07278011-A.

XX

PD 24-OCT-1995.
 XX
 PF 01-APR-1994; 94JP-00085243.
 XX
 PR 01-APR-1994; 94JP-00085243.
 XX
 PA (MORG) MORINAGA MILK IND CO LTD.
 XX
 DR WPI; 1995-400916/51.
 XX
 PT Peptide for treatment of angina pectoris - has low toxicity and is heat
 PT resistant and water soluble.
 XX
 PS Claim 1; Page 11; 12pp; Japanese.
 XX
 CC The present peptide is a bovine lactoferrin derived, angina pectoris
 CC treatative agent. It has low toxicity and side effects, is heat
 CC resistant, water soluble and stable in an aq. soln. . It also requires no
 CC preservative
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KTR 5
 |||
 Db 1 KTR 3

RESULT 36

AAR80266

ID AAR80266 standard; peptide; 11 AA.
 XX
 AC AAR80266;
 XX
 DT 21-FEB-1996 (first entry)
 XX
 DE Anti-parasitic lactoferrin hydrolysate derived peptide.
 XX
 KW Anti-parasitic; lactoferrin; hydrolysate; non-toxic; aquatic animals;
 KW cultured fish; shellfish.
 XX
 OS Homo sapiens.
 XX
 PN JP07145069-A.
 XX
 PD 06-JUN-1995.
 XX
 PF 26-NOV-1993; 93JP-00296281.
 XX
 PR 26-NOV-1993; 93JP-00296281.
 XX
 PA (MORG) MORINAGA MILK IND CO LTD.
 XX
 DR WPI; 1995-237144/31.

XX
PT Drug containing lactoferrin or peptide(s) isolated from its hydrolysates
PT - for prevention or therapy of parasitic diseases in aquatic animals esp.
PT cultured fish and shellfish.
XX
PS Claim 3; Page 12; 14pp; Japanese.
XX
CC AAR79746/60 and AAR80258/70 are non-toxic anti-parasitic peptides derived
CC from lactoferrin hydrolysates. Alone, or in combination with lactoferrins
CC and/or their hydrolysates, the peptides can be used to treat or prevent
CC infectious diseases caused by parasites in aquatic animals, e.g. cultured
CC fish and shellfish
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KTR 5
|||
Db 1 KTR 3

RESULT 37

AAR84537

ID AAR84537 standard; peptide; 11 AA.

XX

AC AAR84537;

XX

DT 06-JUN-1996 (first entry)

XX

DE Hepatitis C virus core antigen (amino acids 8-18).

XX

KW Tailor-made; antigen/antibody specificity exchanger; HIV infection;

KW heavy chain; complementarity determining region; CDR;

KW human immunodeficiency virus; variable loop 3 domain; redirecting;

KW epitope; HCV; hepatitis C virus; core protein.

XX

OS Synthetic.

XX

PN WO9529938-A1.

XX

PD 09-NOV-1995.

XX

PF 27-APR-1995; 95WO-SE0000468.

XX

PR 28-APR-1994; 94SE-00001460.

XX

PA (FERR) FERRING AB.

XX

PI Saellberg M;

XX

DR WPI; 1995-393040/50.

XX

PT Antigen-antibody specificity exchanger - used in a method to redirect a
PT patients antibodies against polio:virus to fight HIV infection in the

PT patient.
 XX
 PS Claim 7; Page 35; 38pp; English.
 XX
 CC An antigen/antibody specificity exchanger comprises an antibody- derived
 CC amino acid sequence (A) which specifically binds to a particular antigen,
 CC linked to an amino acid sequence (C) to which a particular antibody
 CC binds. The present sequence is a preferred example of a type (C) sequence
 CC ; it is an epitope from hepatitis C virus. Preferred type (A) sequences
 CC are complementarity determining regions from e.g. anti-HIV-1 antibodies.
 CC The specificity exchanger can redirect antibodies already present in a
 CC patient and raised against a particular antigen, to fight a different
 CC antigen. For example, it was shown that anti-poliovirus antibodies could
 CC be redirected to fight HIV
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKT 4
 |||
 Db 2 RKT 4

RESULT 38

AAR64598

ID AAR64598 standard; peptide; 11 AA.

XX

AC AAR64598;

XX

DT 25-MAR-2003 (revised)

DT 01-SEP-1995 (first entry)

XX

DE RF-1 peptide 43 from respiratory syncytial virus.

XX

KW antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;

KW human immunodeficiency virus; transmembrane protein; gp41; alpha helix;

KW leucine zipper; DP-185; respiratory syncytial virus; RSV.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "optionally has an amino, acetyl, 9-

FT fluorenylmethoxy-carbonyl, hydrophobic or macromolecular

FT carrier gp. attached"

FT Modified-site 11

FT /note= "optionally has a carboxyl, amido, hydrophobic or

FT macromolecular carrier gp. attached"

XX

PN W09428920-A1.

XX

PD 22-DEC-1994.

XX

PF 07-JUN-1994; 94WO-US005739.

XX
 PR 07-JUN-1993; 93US-00073028.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Bolognesi DP, Matthews TJ, Wild CT, Barney SO, Lambert DM;
 PI Petteway SR;
 XX
 DR WPI; 1995-036105/05.
 XX
 PT Computer search generated synthetic peptides - are inhibitors of HIV
 PT transmission.
 XX
 PS Claim 14; Page 138; 182pp; English.
 XX
 CC AAR64591-623 are peptide derivatives of a 37 mer RF-1 peptide derived
 CC from respiratory syncytial virus (RSV) (AAR64590) which have been
 CC truncated at the amino terminus. The peptides are DP-178 like peptides.
 CC DP-178 corresponds to amino acids 638 to 673 of the HIV-1 isolate LAI
 CC transmembrane protein gp41. It forms a putative alpha helix at the C-
 CC terminal end of the gp41 ectodomain, and complexes with DP-107
 CC (corresponds to amino acids 558-595) which contains a leucine zipper
 CC motif. The peptides complex via non-covalent protein-protein
 CC interactions. The peptide derivatives were identified by a computer
 CC assisted peptide sequence search. The antiviral activity of this peptide
 CC is not stated in the specification. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKS 9
 |||
 Db 5 RKS 7

RESULT 39
 AAR87611
 ID AAR87611 standard; peptide; 11 AA.
 XX
 AC AAR87611;
 XX
 DT 11-JUL-1996 (first entry)
 XX
 DE Lactoferrin-derived anti-fungal peptide.
 XX
 KW Anti-fungal; water soluble; lactoferrin; stable; anti-bacterial;
 KW rapidly metabolised.
 XX
 OS Synthetic.
 XX
 PN JP07309774-A.
 XX
 PD 28-NOV-1995.

XX
 PF 17-MAY-1994; 94JP-00126882.
 XX
 PR 17-MAY-1994; 94JP-00126882.
 XX
 PA (MORG) MORINAGA MILK IND CO LTD.
 XX
 DR WPI; 1996-045320/05.
 XX
 PT Water-soluble anti-fungus agent derived from lactoferrin - has
 PT antibacterial action and is not cytotoxic to animal cells.
 XX
 PS Claim 1; Page 10; 11pp; Japanese.
 XX
 CC AAR87599-R87627 are the active ingredients of an anti-fungal agent. The
 CC agent has anti-bacterial as well as anti-fungal properties but is only
 CC cytotoxic to fungal cells. The agent is water-soluble, hence drugs made
 CC from the agent are rapidly metabolised. The peptides are derived from
 CC fragmented lactoferrin
 XX
 SQ Sequence 11 AA;

 Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 3 KTR 5
 |||
 Db 1 KTR 3

RESULT 40
 AAR91854
 ID AAR91854 standard; peptide; 11 AA.
 XX
 AC AAR91854;
 XX
 DT 20-SEP-1996 (first entry)
 XX
 DE Lactoferrin-derived specific peptide 27, useful for wound healing.
 XX
 KW Bovine lactoferrin; wound healing; skin damage; burn; bedsore.
 XX
 OS Synthetic.
 XX
 PN JP08081387-A.
 XX
 PD 26-MAR-1996.
 XX
 PF 09-SEP-1994; 94JP-00241894.
 XX
 PR 09-SEP-1994; 94JP-00241894.
 XX
 PA (MORG) MORINAGA MILK IND CO LTD.
 XX
 DR WPI; 1996-217187/22.
 XX

PT Wound healing agent comprising specific peptide(s) - is heat resistant,
PT stable in aqueous solution and suitable for oral, external or
PT subcutaneous admin.
XX
PS Claim 1; Page 11; 12pp; Japanese.
XX
CC The present peptide is useful in a novel wound healing agent. The agent
CC is thermostable and stable in aqueous solution. It is administered
CC externally, orally or subcutaneously for treatment of skin damage such as
CC burns or bedsores
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KTR 5
| | |
Db 1 KTR 3

RESULT 41

AAW12602

ID AAW12602 standard; peptide; 11 AA.

XX

AC AAW12602;

XX

DT 08-APR-1997 (first entry)

XX

DE SH2 binding peptide #32.

XX

KW Core peptide; src homology region 2 binding peptide; SH2; cell growth;
KW differentiation; regulation; receptor tyrosine kinase pathway; cancer;
KW signal transduction pathway; non-insulin dependent diabetes;
KW insulin-resistant diabetes.

XX

OS Synthetic.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Disulfide-bond	1. .11
----	----------------	--------

FT	Modified-site	5
----	---------------	---

FT		/label= OTHER
----	--	---------------

FT		/note= "opt. selected from tyrosine, phosphotyrosine,
FT		tyrosine isosteres, and phosphotyrosine isosteres"

FT	Modified-site	10
----	---------------	----

FT		/label= OTHER
----	--	---------------

FT		/note= "opt. selected from tyrosine, phosphotyrosine,
FT		tyrosine isosteres, and phosphotyrosine isosteres, esp.
FT		phosphotyrosine"

FT	Modified-site	11
----	---------------	----

FT		/note= "amidated C-terminal"
----	--	------------------------------

XX

PN W09623813-A1.

XX

PD 08-AUG-1996.

XX

PF 31-JAN-1996; 96WO-US001544.
 XX
 PR 01-FEB-1995; 95US-00382100.
 XX
 PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
 XX
 PI Patel DV, Gordeev MF, Gordon E, Grove JR, Hart CP, Kim MH;
 PI Szardenings AK;
 XX
 DR WPI; 1996-371373/37.
 XX
 PT Peptide(s) which bind to SH2 domains - are used to treat diseases
 PT associated with aberrant cell growth, differentiation or regulation
 PT associated with defects in receptor tyrosine kinase pathways.
 XX
 PS Claim 14; Page 118; 203pp; English.
 XX
 CC The sequences given in AAW12571-614 represent src homology region 2 (SH2)
 CC binding peptides which contain a core peptide which corresponds to the
 CC formula: Z7-X-Z8-X X = any D- or L- amino acid; Z7 = phosphotyrosine or
 CC its isostere; Z8 = asparagine or its isostere; the amino terminus is
 CC acylated, and the peptide is less than 14 residues in length, with the
 CC proviso that if Z7 is phosphotyrosine and Z8 is asparagine, then the
 CC peptide is not GDGZ7XZ8XPPLL. These SH2 binding peptides are used to
 CC treat of diagnose diseases associated with aberrant cell growth,
 CC differentiation or regulation which is associated with defects in
 CC receptor tyrosine kinase pathways, by partially blocking or inhibiting a
 CC cellular signal transduction pathway. The disease may be cancer, a
 CC developmental or differentiation disease or insulin-resistant (or non-
 CC insulin dependent) diabetes
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RER 7
 |||
 Db 2 RER 4

RESULT 42

AAW05350

ID AAW05350 standard; peptide; 11 AA.

XX

AC AAW05350;

XX

DT 30-APR-1997 (first entry)

XX

DE Residues 363-373 of p53.

XX

KW Human; p53; cell proliferation; cell death; regulator; tumour; psoriasis;
 KW negative regulatory region; DNA damaging agent; transplant rejection;
 KW abnormal cell proliferation; atherosclerosis; cancer; autoimmune disease;
 KW arterial restenosis; immune response; apoptosis; inducer; therapy;
 KW proliferating lymphocytes.

XX
 OS Homo sapiens.
 XX
 PN WO9625434-A1.
 XX
 PD 22-AUG-1996.
 XX
 PF 16-FEB-1996; 96WO-US001535.
 XX
 PR 16-FEB-1995; 95US-00392542.
 XX
 PA (WIST-) WISTAR INST.
 PA (FARB) BAYER CORP.
 XX
 PI Halazonetis T, Hartwig W;
 XX
 DR WPI; 1996-393345/39.
 XX
 PT New human p53-isomorphic peptide(s) and peptido:mimetic cpds. - used for
 PT activating p53 function, e.g. for treating tumours, cancers, psoriasis,
 PT etc.
 XX
 PS Claim 2; Page 35; 55pp; English.
 XX
 CC AAW05350-W05364 represent the p53 (see AAW05344 for full length wild type
 CC sequence) peptides of the invention. The p53 protein functions to
 CC regulate cell proliferation and cell death, and is mutated in more than
 CC half of all human tumours. These sequences are used to activate the DNA
 CC binding activity of wild type p53, and p53 mutants (see AAW05345-W05349).
 CC The peptides of the invention consist of at least four sequential amino
 CC acids from a negative regulatory region which maps to residues 361-383 of
 CC p53. These sequences preferably contain four amino acids from a non-human
 CC p53 sequence, contain D-form amino acids, and can also be cyclic
 CC peptides. The sequences retain the structural characteristics of the
 CC original peptides, but the modifications render them less susceptible to
 CC cleavage by proteases and exopeptidases. As these sequences activate p53
 CC DNA binding, they can be used to identify p53 mutants. The peptides can
 CC also be used for treating a patient with a tumour expressing a p53 mutant
 CC whose ability to bind DNA may be activated by one of the peptides. They
 CC can also be used for treating conditions such as exposure to DNA damaging
 CC agents, abnormal cell proliferation characteristic of psoriasis,
 CC atherosclerosis, cancer, arterial restenosis, autoimmune diseases and
 CC undesirable immune responses accompanying rejection of a transplant. The
 CC peptides can also induce apoptosis of specific cells, such as
 CC proliferating lymphocytes
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KSK 10
 |||
 Db 8 KSK 10

RESULT 43

AAW05374

ID AAW05374 standard; peptide; 11 AA.

XX

AC AAW05374;

XX

DT 30-APR-1997 (first entry)

XX

DE Reverse D peptide p53RDp363-373.

XX

KW Human; p53; cell proliferation; cell death; regulator; tumour; psoriasis;

KW negative regulatory region; DNA damaging agent; transplant rejection;

KW abnormal cell proliferation; atherosclerosis; cancer; autoimmune disease;

KW arterial restenosis; immune response; apoptosis; inducer; therapy;

KW proliferating lymphocytes.

XX

OS Synthetic.

XX

PN WO9625434-A1.

XX

PD 22-AUG-1996.

XX

PF 16-FEB-1996; 96WO-US001535.

XX

PR 16-FEB-1995; 95US-00392542.

XX

PA (WIST-) WISTAR INST.

PA (FARB) BAYER CORP.

XX

PI Halazonetis T, Hartwig W;

XX

DR WPI; 1996-393345/39.

XX

PT New human p53-isomorphic peptide(s) and peptido:mimetic cpds. - used for

PT activating p53 function, e.g. for treating tumours, cancers, psoriasis,

PT etc.

XX

PS Disclosure; Page 13; 55pp; English.

XX

CC AAW05365-W05374 represent examples of the p53 (see AAW05344 for full
CC length wild type sequence) peptides of the invention. These sequences all
CC have additions or deletions of residues from the wild type peptide
CC fragments of the invention (see AAW05350-W05364). The p53 protein
CC functions to regulate cell proliferation and cell death, and is mutated
CC in more than half of all human tumours. These sequences are used to
CC activate the DNA binding activity of wild type p53, and p53 mutants (see
CC AAW05345-W05349). The peptides of the invention consist of at least four
CC sequential amino acids from a negative regulatory region which maps to
CC residues 361-383 of p53. These sequences preferably contain four amino
CC acids from a non-human p53 sequence, contain D-form amino acids, and can
CC also be cyclic peptides. The sequences retain the structural
CC characteristics of the original peptides, but the modifications render
CC them less susceptible to cleavage by proteases and exopeptidases. As
CC these sequences activate p53 DNA binding, they can be used to identify
CC p53 mutants. The peptides can also be used for treating a patient with a
CC tumour expressing a p53 mutant whose ability to bind DNA may be activated
CC by one of the peptides. They can also be used for treating conditions

CC such as exposure to DNA damaging agents, abnormal cell proliferation
CC characteristic of psoriasis, atherosclerosis, cancer, arterial
CC restenosis, autoimmune diseases and undesirable immune responses
CC accompanying rejection of a transplant. The peptides can also induce
CC apoptosis of specific cells, such as proliferating lymphocytes
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KSK 10
|||
Db 2 KSK 4

RESULT 44

AAW03991

ID AAW03991 standard; peptide; 11 AA.

XX

AC AAW03991;

XX

DT 30-APR-1997 (first entry)

XX

DE pY peptide liagnd #2.

XX

KW Polymerase chain reaction; PCR; amplify; primer; chicken; src;

KW SH2 domain; DET1; DET2; erythropoiesis; anaemia; haematopoiesis;

KW antagonist.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 4

FT /note= "Phosphorylated Tyr"

XX

PN EP728482-A2.

XX

PD 28-AUG-1996.

XX

PF 07-FEB-1996; 96EP-00200269.

XX

PR 10-FEB-1995; 95US-00386381.

PR 07-MAR-1995; 95US-00400220.

PR 30-JUN-1995; 95US-00497357.

PR 11-OCT-1995; 95US-00540680.

PR 29-DEC-1995; 95US-00581089.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Dunnington DJ;

XX

DR WPI; 1996-386024/39.

XX

PT Use of selective antagonist of haematopoietic acid phosphatase SH2 domain

PT - with no significant affinity for other SH2 domains, to increase

PT erythropoiesis and haematopoiesis, esp. for treatment of anaemia.
 XX
 PS Example; Page 21; 46pp; English.
 XX
 CC The sequences given in AAW03990-94 represent phosphorylated Tyr peptides
 CC which were used in the isolation of a compound for improving
 CC erythropoiesis. The isolated compound may be used for the treatment of
 CC anaemia or to enhance haematopoiesis. The isolated compound antagonises
 CC the hcp SH2 domain without side effects caused by non-specific inhibition
 CC of other SH2 domains
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SKD 11
 |||
 Db 8 SKD 10

RESULT 45

AAR96813

ID AAR96813 standard; peptide; 11 AA.

XX

AC AAR96813;

XX

DT 29-NOV-1996 (first entry)

XX

DE Human laminin b2 fragment, homologous to N.gonorrhoeae MS11 IgaP.

XX

KW IgA protease precursor; IPP; bacterial polyprotein; autoimmune;

KW viral infection; rheumatoid arthritis; AIDS; meningococcal bacteria;

KW human laminin b2; Neisseria gonorrhoeae.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Region	1. .5
----	--------	-------

FT		/note= "identical to sequence in Neisseria gonorrhoeae IgaP"
----	--	--

FT	Region	7
----	--------	---

FT		/note= "identical to corresponding residue in Neisseria gonorrhoeae IgaP"
----	--	---

FT	Region	10. .11
----	--------	---------

FT		/note= "identical to sequence in Neisseria gonorrhoeae IgaP"
----	--	--

XX

PN WO9609395-A2.

XX

PD 28-MAR-1996.

XX

PF 21-SEP-1995; 95WO-EP003726.

XX

PR 21-SEP-1994; 94DE-04433708.

XX

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Meyer TF, Pohlner J, Beck SC, Jose J, Woelk U, Lorenzen DR;
 PI Oetzelberger KB;
 XX
 DR WPI; 1996-188456/19.
 XX
 PT Medicaments for treating auto-immune or viral diseases - contg.
 PT substances interfering with bacterial poly:protein function.
 XX
 PS Claim 32; Fig 2; 117pp; German.
 XX
 CC The present sequence from human laminin b2 has homology to a cleavage
 CC product from the IgaP domain of the precursor of IgA-protease polyprotein
 CC (IPP) of Neisseria gonorrhoeae strain MS11. The Neisseria IPP has been
 CC implicated in rheumatoid arthritis and other auto-immune diseases. The
 CC polyprotein also activates proviruses, including HIV. Substances which
 CC interfere with the function of IPP from Neisseria will be useful for
 CC treating associated autoimmune diseases and viral infections. Peptides
 CC comprising the homology region sequences, whether from Neisseria or from
 CC humans, are claimed
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
 |||
 Db 3 ARK 5

RESULT 46
 AAR96812

ID AAR96812 standard; peptide; 11 AA.
 XX
 AC AAR96812;
 XX
 DT 16-OCT-2003 (revised)
 DT 29-NOV-1996 (first entry)
 XX
 DE N.gonorrhoeae MS11 IgaP region, homologous to human laminin b2.
 XX
 KW IgA protease precursor; IPP; bacterial polyprotein; autoimmune;
 KW viral infection; rheumatoid arthritis; AIDS; meningococcal bacteria;
 KW human laminin b2.
 XX
 OS Neisseria gonorrhoeae; MS11.
 XX
 FH Key Location/Qualifiers
 FT Region 1. .5
 FT /note= "identical to sequence in human laminin b2"
 FT Region 7
 FT /note= "identical to corresponding residue in human
 FT laminin b2"
 FT Region 10. .11

FT /note= "identical to sequence in human laminin b2"
 XX
 PN WO9609395-A2.
 XX
 PD 28-MAR-1996.
 XX
 PF 21-SEP-1995; 95WO-EP003726.
 XX
 PR 21-SEP-1994; 94DE-04433708.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Meyer TF, Pohlner J, Beck SC, Jose J, Woelk U, Lorenzen DR;
 PI Oetzelberger KB;
 XX
 DR WPI; 1996-188456/19.
 XX
 PT Medicaments for treating auto-immune or viral diseases - contg.
 PT substances interfering with bacterial poly:protein function.
 XX
 PS Claim 32; Fig 2; 117pp; German.
 XX
 CC The present sequence is a cleavage product from the IgaP domain of the
 CC precursor of IgA-protease polyprotein (IPP) of Neisseria gonorrhoeae
 CC strain MS11. The Neisseria IPP has marked homology to certain human
 CC proteins and has been implicated in rheumatoid arthritis and other auto-
 CC immune diseases. The polyprotein also activates proviruses, including
 CC HIV. Substances which interfere with the function of IPP from Neisseria
 CC will be useful for treating associated autoimmune diseases and viral
 CC infections. The present peptide is homologous to human laminin b2.
 CC (Updated on 16-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
 |||
 Db 3 ARK 5

RESULT 47

AAR96834

ID AAR96834 standard; peptide; 11 AA.

XX

AC AAR96834;

XX

DT 16-OCT-2003 (revised)

DT 29-NOV-1996 (first entry)

XX

DE N.gonorrhoeae Iga alphas region, homologous to human Nfh protein.

XX

KW IgA protease precursor; IPP; bacterial polyprotein; autoimmune;

KW viral infection; rheumatoid arthritis; AIDS; meningococcal bacteria;

KW human neurofilament triplet h protein; Nfh.

```

XX
OS   Neisseria gonorrhoeae; MS11.
XX
FH   Key          Location/Qualifiers
FT   Region       1. .3
FT               /note= "identical to sequence in human neurofilament
FT               triplet h protein"
FT   Region       5. .7
FT               /note= "identical to sequence in human neurofilament
FT               triplet h protein"
FT   Region       10. .11
FT               /note= "identical to sequence in human neurofilament
FT               triplet h protein"
XX
PN   WO9609395-A2.
XX
PD   28-MAR-1996.
XX
PF   21-SEP-1995; 95WO-EP003726.
XX
PR   21-SEP-1994; 94DE-04433708.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Meyer TF, Pohlner J, Beck SC, Jose J, Woelk U, Lorenzen DR;
PI   Oetzelberger KB;
XX
DR   WPI; 1996-188456/19.
XX
PT   Medicaments for treating auto-immune or viral diseases - contg.
PT   substances interfering with bacterial poly:protein function.
XX
PS   Claim 32; Fig 2; 117pp; German.
XX
CC   The present sequence is a cleavage product from the Iga alpha 1 domain of
CC   the precursor of IgA-protease polyprotein (IPP) of N.gonorrhoeae strain
CC   MS11. The Neisseria IPP has marked homology to certain human proteins and
CC   has been implicated in rheumatoid arthritis and other auto-immune
CC   diseases. The polyprotein also activates proviruses, including HIV.
CC   Substances which interfere with the function of IPP from Neisseria will
CC   be useful for treating associated autoimmune diseases and viral
CC   infections. The present peptide is homologous to a region from human
CC   neurofilament triplet h protein. (Updated on 16-OCT-2003 to standardise
CC   OS field)
XX
SQ   Sequence 11 AA;

      Query Match          27.3%; Score 3; DB 2; Length 11;
      Best Local Similarity 100.0%; Pred. No. 8.8e+03;
      Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY          1 ARK 3
           |||
Db          7 ARK 9

```

RESULT 48

AAR81803

ID AAR81803 standard; peptide; 11 AA.

XX

AC AAR81803;

XX

DT 27-AUG-2003 (revised)

DT 10-JUL-1996 (first entry)

XX

DE E-Dex integrin inhibitor 1 epitope (aa78-88).

XX

KW Integrin inhibitor; E-Dex; neutrophil; leukocyte; trans-migration;

KW cell adhesion; tick-derived antiinflammatory protein; Ixodes pacificus;

KW Amblyomma americanum; epitope; antibody; immunoassay.

XX

OS Ixodida sp.

XX

PN WO9605304-A1.

XX

PD 22-FEB-1996.

XX

PF 08-AUG-1995; 95WO-US010138.

XX

PR 09-AUG-1994; 94US-00287730.

XX

PA (ATHE-) ATHENA NEUROSCIENCES INC.

XX

PI Bard F, Yednock TA, Keim PS, Basi GS;

XX

DR WPI; 1996-139700/14.

XX

PT Tick derived anti-inflammatory proteins E-Dex and Y/A-Dex - used to

PT inhibit leukocyte trans-migration and in the treatment of inflammatory

PT disease.

XX

PS Disclosure; Page 40; 76pp; English.

XX

CC Preferred polypeptide epitopes (AAR81797-804) of tick-derived

CC antiinflammatory protein E-Dex (see also AAR81794), or integrin inhibitor

CC 1, are used to raise anti-E-Dex polyclonal or monoclonal antibodies

CC useful as research reagents for titration of E-Dex inhibitory activity in

CC assays or for immunoassay of E-Dex in samples. The epitopes may have C-

CC or N-terminal extensions or be fused to other protein sequences e.g.

CC albumin. (Updated on 27-AUG-2003 to correct OS field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TRE 6

|||

Db 9 TRE 11

RESULT 49

AAR90709

ID AAR90709 standard; peptide; 11 AA.
 XX
 AC AAR90709;
 XX
 DT 21-AUG-1996 (first entry)
 XX
 DE Residues 496-506 of Fc region of human IgE.
 XX
 KW T cell; epitope; immunogen; histamine; antibody; therapy; allergy; assay;
 KW rye grass allergy; hayfever; sensitivity; allergen; Lolium perenne; IgE;
 KW Lol pI; human.
 XX
 OS Synthetic.
 XX
 PN WO9600238-A1.
 XX
 PD 04-JAN-1996.
 XX
 PF 26-JUN-1995; 95WO-GB001493.
 XX
 PR 24-JUN-1994; 94GB-00012714.
 XX
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
 XX
 PI Lewin IV, Bungy A;
 XX
 DR WPI; 1996-068831/07.
 XX
 PT Novel T cell epitope of rye grass allergen - used in an immunogen for
 PT determination of sensitivity to rye grass pollen and in the treatment of
 PT hay-fever.
 XX
 PS Disclosure; Page 5; 50pp; English.
 XX
 CC This sequence represents residues 496-506 of the human IgE Fc region, and
 CC covers the Cepsilon4 domain. This sequence can be used as a histamine
 CC releasing peptide in an immunogen of the invention. This sequence
 CC comprises a cationic N-terminal head and a hydrophobic C-terminal tail,
 CC together with a residue capable of eliciting antibodies against a T cell
 CC motif (see AAR90704) containing peptide (see AAR90705-R90707). The
 CC peptides and immunogens are used in a medicament for the treatment or
 CC prophylaxis of allergies, particularly for rye grass allergy or hayfever.
 CC They may also be used in assays to determine sensitivity to rye grass
 CC allergens, for determination of hayfever sufferance, or to assay specific
 CC T cell populations sensitive to rye grass allergens such as the Lolium
 CC perenne protein Lol pI
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKT 4
 |||
 Db 1 RKT 3

RESULT 50

AAW02115

ID AAW02115 standard; peptide; 11 AA.

XX

AC AAW02115;

XX

DT 29-OCT-1996 (first entry)

XX

DE Biotinylated pY peptide ligand for p85 SH2 domain.

XX

KW Bone resorption disease; osteoporosis; src SH2 domain antagonist;

KW src homology 2 domain; p85.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 4

FT /label= OTHER

FT /note= "phosphotyrosine"

XX

PN EP727211-A1.

XX

PD 21-AUG-1996.

XX

PF 07-FEB-1996; 96EP-00200270.

XX

PR 10-FEB-1995; 95US-00386381.

PR 07-MAR-1995; 95US-00400220.

PR 30-JUN-1995; 95US-00497357.

PR 11-OCT-1995; 95US-00541080.

PR 29-DEC-1995; 95US-00580868.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Dunnington DJ;

XX

DR WPI; 1996-372674/38.

XX

PT Use of selective src SH2 domain ligand - to prepare medicament for

PT treating bone resorption disease.

XX

PS Example 11; Page 21; 47pp; English.

XX

CC Biotinylated pY peptides (AAW02114-18) contg. an aminocaproic acid linker

CC are used in binding assays to determine the ability of cpds. to

CC selectively inhibit the binding of the SH2 domain of a human protein to

CC its respective pY peptide; the peptide given in AAW02115 was used for p85

CC SH2. The SH2 domains were expressed as fusion proteins (see also AAW02119

CC -21 and AAW02124-27) in E. coli for use in the assays. Cpds. that

CC selectively inhibit the human src SH2 domain can be used to treat bone

CC resorption diseases such as osteoporosis

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SKD 11
| | |
Db 8 SKD 10

RESULT 51

AAW09653

ID AAW09653 standard; peptide; 11 AA.

XX

AC AAW09653;

XX

DT 25-MAR-2003 (revised)

DT 20-MAY-1997 (first entry)

XX

DE Labelled peptide substrate used in enzyme activity assay.

XX

KW Enzyme activity; assay; measurement; label; rhodamine; dansyl;

KW non-radioactive; electrophoretic separation; protein kinase; protease;

KW phosphatase.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "labelled with rhodamine B detection tag"

XX

PN US5580747-A.

XX

PD 03-DEC-1996.

XX

PF 21-JAN-1994; 94US-00185448.

XX

PR 12-NOV-1991; 91US-00791928.

XX

PA (PROM-) PROMEGA CORP.

XX

PI White DH, Shultz JW;

XX

DR WPI; 1997-033568/03.

XX

PT Non:radioactive assay for measuring enzyme activity - involving

PT electrophoretic sepn. of labelled cleavage prod. from labelled peptide

PT substrate.

XX

PS Claim 5; Col 39-40; 35pp; English.

XX

CC AAW09653 is a peptide substrate used in a non-radioactive assay for
CC measuring enzyme activity. The assay comprises incubating the enzyme with
CC the labelled peptide substrate to form a labelled peptide product;
CC separating the product from the substrate by agarose gel electrophoresis
CC and measuring the amount of product by detecting the label by
CC fluorescence or chemiluminescence. The assay can be performed rapidly and
CC with great sensitivity. This peptide is especially for determining
CC protein kinase C activity, e.g. to study its function in metabolism or to
CC screen for potential inhibitors. (Updated on 25-MAR-2003 to correct PF

CC field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RKS 9
|||
Db 5 RKS 7

RESULT 52

AAW25587

ID AAW25587 standard; peptide; 11 AA.

XX

AC AAW25587;

XX

DT 25-MAR-2003 (revised)

DT 10-NOV-1997 (first entry)

XX

DE Synthetic hepatitis peptide #29.

XX

KW Functional surrogate; analyte; affinity receptor; immunoreactive group;
KW mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia;
KW cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin;
KW pregnancy; infectious disease; ferritin; myosin light chain; troponin;
KW follicle stimulating hormone; human; growth hormone; immunoglobulin E;
KW prolactin; parathyroid hormone; placental lactogen; hepatitis antigen;
KW antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus;
KW Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen;
KW carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /label= Acp

FT /note= "the amino group of this residue is attached to
the thiol group of Cys11 via a -CO-CH2- bridge"

FT Modified-site 2

FT /note= "the epsilon amine group is biotinylated"

FT Modified-site 11

FT /note= "the thiol group of this residue is attached to
the amino group Acpl via a -CO-CH2- bridge, amidated C
terminal"

XX

PN W09641172-A1.

XX

PD 19-DEC-1996.

XX

PF 07-JUN-1996; 96WO-US010498.

XX

PR 07-JUN-1995; 95US-00476375.

XX

PA (CYTO-) CYTOGEN CORP.

XX
 PI Lee-Owen FV, Carter JM;
 XX
 DR WPI; 1997-077284/07.
 XX
 PT Labelled functional surrogate of an analyte - useful as competitor
 PT molecule in affinity assays, esp. for detecting large macromolecules such
 PT as ferritin.
 XX
 PS Claim 51; Page 28; 156pp; English.
 XX
 CC This sequence represents a synthetic hepatitis peptide which was used as
 CC a functional surrogate in the conjugate of the invention. The novel
 CC labelled conjugate comprises at least one label attached to a functional
 CC surrogate of an analyte of interest. The surrogate is capable of
 CC competing effectively with the analyte for a limiting amount of an
 CC affinity receptor for the analyte. The conjugate exhibits an activity
 CC that is altered upon interaction with the affinity receptor and this
 CC activity can be measured and related to the amount of the analyte present
 CC in a sample. Functional surrogates such as this have an immunoreactive
 CC group that allows the surrogate to compete effectively and with the
 CC analyte for a limiting amount of its affinity receptor. Functional
 CC surrogates are able to mimic naturally occurring analytes. They can be
 CC labelled for use in standard competitive affinity assays (esp. homogenous
 CC immunoassays) for detecting large macromolecules such as polypeptides,
 CC polysaccharides, polynucleotides, glycoproteins and lipid-containing
 CC macromolecules, as well as small haptens. Typical diagnostic analytes for
 CC detection include cardiac or tumour markers, allergens, hormones related
 CC to fertility-pregnancy or analytes associated with infectious disease. In
 CC particular, the assays are useful for detecting ferritin, follicle
 CC stimulating hormone, human growth hormone, immunoglobulin E, prolactin,
 CC parathyroid hormone, human placental lactogen, hepatitis antigens or
 CC antibodies against them, human chorionic gonadotropin, human luteinising
 CC hormone, cytomegalovirus, Chlamydia, Streptococcus a, rubella,
 CC toxoplasma, herpes virus, DK-MB, myoglobin, myosin light chain, troponin,
 CC carcinoembryonic antigen, alpha-fetoprotein, prostate-specific antigen
 CC and CA125 (a tumour marker). (Updated on 25-MAR-2003 to correct PI
 CC field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KTR 5
 |||
 Db 2 KTR 4

RESULT 53
 AAW25586
 ID AAW25586 standard; peptide; 11 AA.
 XX
 AC AAW25586;
 XX
 DT 25-MAR-2003 (revised)

DT 10-NOV-1997 (first entry)
 XX
 DE Synthetic hepatitis peptide #28.
 XX
 KW Functional surrogate; analyte; affinity receptor; immunoreactive group;
 KW mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia;
 KW cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin;
 KW pregnancy; infectious disease; ferritin; myosin light chain; troponin;
 KW follicle stimulating hormone; human; growth hormone; immunoglobulin E;
 KW prolactin; parathyroid hormone; placental lactogen; hepatitis antigen;
 KW antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus;
 KW Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen;
 KW carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= Acp
 FT /note= "the amino group of this residue is attached to
 FT the thiol group of Cys11 via a -CO-CH2- bridge"
 FT Modified-site 11
 FT /note= "the thiol group of this residue is attached to
 FT the amino group Acpl via a -CO-CH2- bridge, amidated C
 FT terminal"
 XX
 PN WO9641172-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US010498.
 XX
 PR 07-JUN-1995; 95US-00476375.
 XX
 PA (CYTO-) CYTOGEN CORP.
 XX
 PI Lee-Owen FV, Carter JM;
 XX
 DR WPI; 1997-077284/07.
 XX
 PT Labelled functional surrogate of an analyte - useful as competitor
 PT molecule in affinity assays, esp. for detecting large macromolecules such
 PT as ferritin.
 XX
 PS Claim 51; Page 28; 156pp; English.
 XX
 CC This sequence represents a synthetic hepatitis peptide which was used as
 CC a functional surrogate in the conjugate of the invention. The novel
 CC labelled conjugate comprises at least one label attached to a functional
 CC surrogate of an analyte of interest. The surrogate is capable of
 CC competing effectively with the analyte for a limiting amount of an
 CC affinity receptor for the analyte. The conjugate exhibits an activity
 CC that is altered upon interaction with the affinity receptor and this
 CC activity can be measured and related to the amount of the analyte present
 CC in a sample. Functional surrogates such as this have an immunoreactive
 CC group that allows the surrogate to compete effectively and with the
 CC analyte for a limiting amount of its affinity receptor. Functional

CC surrogates are able to mimic naturally occurring analytes. They can be
CC labelled for use in standard competitive affinity assays (esp. homogenous
CC immunoassays) for detecting large macromolecules such as polypeptides,
CC polysaccharides, polynucleotides, glycoproteins and lipid-containing
CC macromolecules, as well as small haptens. Typical diagnostic analytes for
CC detection include cardiac or tumour markers, allergens, hormones related
CC to fertility-pregnancy or analytes associated with infectious disease. In
CC particular, the assays are useful for detecting ferritin, follicle
CC stimulating hormone, human growth hormone, immunoglobulin E, prolactin,
CC parathyroid hormone, human placental lactogen, hepatitis antigens or
CC antibodies against them, human chorionic gonadotropin, human luteinising
CC hormone, cytomegalovirus, Chlamydia, Streptococcus a, rubella,
CC toxoplasma, herpes virus, DK-MB, myoglobin, myosin light chain, troponin,
CC carcinoembryonic antigen, alpha-fetoprotein, prostate-specific antigen
CC and CA125 (a tumour marker). (Updated on 25-MAR-2003 to correct PI
CC field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KTR 5
|||
Db 2 KTR 4

RESULT 54

AAW15675

ID AAW15675 standard; peptide; 11 AA.

XX

AC AAW15675;

XX

DT 25-MAR-2003 (revised)

DT 11-JUN-1997 (first entry)

XX

DE Platelet aggregation inhibitor #100.

XX

KW Platelet aggregation inhibitor; RGD analogue; cyclic peptide; fibrinogen;

KW hydrophobically enhanced analogue; blood platelet; endothelial surface;

KW blood vessel; serum protein; GP IIb/IIIa glycoprotein complex; integrin;

KW plasma membrane; thrombosis; cell adhesion receptor; fibronectin;

KW vitronectin receptor; vascular graft occlusion; therapy.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 2. .10

FT /note= "forms peptide bond to create cyclic peptide"

FT Modified-site 2

FT /label= Orn

XX

PN US5612311-A.

XX

PD 18-MAR-1997.

XX

PF 22-DEC-1994; 94US-00363963.

XX

PR 06-APR-1990; 90US-00506444.

PR 05-APR-1991; 91US-00681119.

PR 14-APR-1993; 93US-00050736.

PR 02-MAR-1994; 94US-00204817.

XX

PA (LJOL-) LA JOLLA CANCER RES FOUND.

XX

PI Craig WS, Lukeman DS, Cheng S, Tschopp JF, Pierschbacher MD;

XX

DR WPI; 1997-192139/17.

XX

PT RGD-contg. peptide(s) that inhibit platelet aggregation - useful for
PT treating thrombosis.

XX

PS Example 5; Col 79; 50pp; English.

XX

CC AAW15576-W15695 represent platelet aggregation inhibitors. All of these
CC sequences are hydrophobically enhanced RGD peptide analogues. The
CC interaction of blood platelets with the endothelial surface of injured
CC blood vessels and with other platelets (platelet aggregation) is a major
CC factor in the course of development of thrombi. Thrombosis is a serious
CC condition which can cause tissue damage and eventually death (if
CC untreated). Platelet aggregation is dependent upon the binding of
CC fibrinogen and other serum proteins to the GP IIb/IIIa glycoprotein
CC complex on the platelet plasma membrane. GP IIb/IIIa is a member of the
CC integrin family of cell adhesion receptors, which are known to recognise
CC a RGD tripeptide recognition sequence. The peptides inhibit platelet
CC aggregation without prolonging bleeding time. These sequences have high
CC affinity for the IIb/IIIa receptor and low affinity for the fibronectin
CC and vitronectin receptors. The peptides are used as platelet aggregation
CC inhibitors for treating thrombosis and vascular graft occlusion. (Updated
CC on 25-MAR-2003 to correct PF field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RER 7

|||

Db 9 RER 11

RESULT 55

AAW22738

ID AAW22738 standard; peptide; 11 AA.

XX

AC AAW22738;

XX

DT 12-MAR-1998 (first entry)

XX

DE Linking sequence from metastasis inhibitor.

XX

KW Chimeric; human; urinary trypsin; inhibitor; HI-8; cancer; metastasis;

KW G-domain; urokinase; prevention; leukaemia; lymphoma.
 XX
 OS Synthetic.
 XX
 PN WO9725422-A1.
 XX
 PD 17-JUL-1997.
 XX
 PF 06-JAN-1997; 97WO-JP000008.
 XX
 PR 08-JAN-1996; 96JP-00001059.
 XX
 PA (NISP) NISSIN FOOD PROD CO LTD.
 XX
 PI Kobayashi H, Terao T, Sugino D, Okushima M;
 XX
 DR WPI; 1997-372862/34.
 XX
 PT Chimeric protein which inhibits development of metastases in cancer -
 PT contains urinary trypsin inhibitor carboxy-terminal domain linked to
 PT urokinase G-domain.
 XX
 PS Claim 2; Page 68; 97pp; Japanese.
 XX
 CC A novel chimeric protein contains the carboxy-terminal domain of human
 CC urinary trypsin inhibitor (HI-8), which inhibits cancer cell metastasis,
 CC linked to a peptide containing the G-domain of urokinase (AAW22742),
 CC which specifically binds the excess urokinase receptor expressed in
 CC cancer cells. The chimeric protein has the amino-terminal AAW22734, the
 CC carboxy-terminal AAW22735 and a linking sequence selected from AAW22736-
 CC 39 or partial sequences derived from these, specifically AAW38130-63. The
 CC chimeric protein may also have additional amino-terminal sequences
 CC selected from AAW22740 or 9 partial sequences derived from this, and/or
 CC additional carboxy-terminal sequences selected from AAW22743 or 10
 CC partial sequences derived from this. The chimeric protein can be used to
 CC prevent metastasis in, e.g. cancer of the lung, kidney, pancreas,
 CC stomach, colon, rectum, ovary, uterus, brain, skin, muscle, breast or
 CC prostate, and in leukaemia or lymphoma
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KSK 10
 |||
 Db 4 KSK 6

RESULT 56
 AAW38140
 ID AAW38140 standard; peptide; 11 AA.
 XX
 AC AAW38140;
 XX
 DT 12-MAR-1998 (first entry)

XX
 DE Linking sequence from metastasis inhibitor.
 XX
 KW Chimeric; human; urinary trypsin; inhibitor; HI-8; cancer; metastasis;
 KW G-domain; urokinase; prevention; leukaemia; lymphoma.
 XX
 OS Synthetic.
 XX
 PN WO9725422-A1.
 XX
 PD 17-JUL-1997.
 XX
 PF 06-JAN-1997; 97WO-JP000008.
 XX
 PR 08-JAN-1996; 96JP-00001059.
 XX
 PA (NISP) NISSIN FOOD PROD CO LTD.
 XX
 PI Kobayashi H, Terao T, Sugino D, Okushima M;
 XX
 DR WPI; 1997-372862/34.
 XX
 PT Chimeric protein which inhibits development of metastases in cancer -
 PT contains urinary trypsin inhibitor carboxy-terminal domain linked to
 PT urokinase G-domain.
 XX
 PS Claim 3; Page 70; 97pp; Japanese.
 XX
 CC A novel chimeric protein contains the carboxy-terminal domain of human
 CC urinary trypsin inhibitor (HI-8), which inhibits cancer cell metastasis,
 CC linked to a peptide containing the G-domain of urokinase (AAW22742),
 CC which specifically binds the excess urokinase receptor expressed in
 CC cancer cells. The chimeric protein has the amino-terminal AAW22734, the
 CC carboxy-terminal AAW22735 and a linking sequence selected from AAW22736-
 CC 39 or partial sequences derived from these, specifically AAW38130-63. The
 CC chimeric protein may also have additional amino-terminal sequences
 CC selected from AAW22740 or 9 partial sequences derived from this, and/or
 CC additional carboxy-terminal sequences selected from AAW22743 or 10
 CC partial sequences derived from this. The chimeric protein can be used to
 CC prevent metastasis in, e.g. cancer of the lung, kidney, pancreas,
 CC stomach, colon, rectum, ovary, uterus, brain, skin, muscle, breast or
 CC prostate, and in leukaemia or lymphoma
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KSK 10
 |||
 Db 4 KSK 6

RESULT 57
 AAW39576
 ID AAW39576 standard; peptide; 11 AA.

XX
 AC AAW39576;
 XX
 DT 11-JUN-1998 (first entry)
 XX
 DE Human Influenza M derived peptide (residues 41-51).
 XX
 KW T cell epitope; immune response; human leukocyte antigen; HLA Class I;
 KW vaccine; immunogenic; major histocompatibility complex; MHC; B cell;
 KW disease; anti-tumour; anti-viral.
 XX
 OS Influenza virus.
 XX
 PN WO9741440-A1.
 XX
 PD 06-NOV-1997.
 XX
 PF 28-APR-1997; 97WO-NL000229.
 XX
 PR 26-APR-1996; 96EP-00201145.
 PR 23-DEC-1996; 96EP-00203670.
 XX
 PA (UYLE-) RIJKSUNIV LEIDEN.
 PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
 XX
 PI Van Der Burg SH, Kast WM, Toes REM, Offringa R, Melief CJM;
 XX
 DR WPI; 1997-549891/50.
 XX
 PT Method of selecting T cell peptide epitope(s) - by measuring the
 PT stability of HLA class I-peptide complexes on intact B cells.
 XX
 PS Example 3; Page 74; 109pp; English.
 XX
 CC Peptides AAW39430-W39734 are used in a novel method for the selection of
 CC immunogenic T-cell peptide epitopes present in polypeptide antigens. The
 CC method involves the identification of peptide sequences capable of
 CC binding to an HLA (human leukocyte antigen) class I molecule and
 CC measuring the binding of this epitope peptide to the HLA class I peptide.
 CC The stability of binding of the peptide and MHC (major histocompatibility
 CC complex) class I molecule is measured on intact human B cells carrying
 CC the MHC molecule at their cell surfaces. The method can be used to select
 CC peptide epitopes for generating vaccines against a disease associated
 CC with the polypeptide, e.g. cancers or AIDS. The peptide epitopes are
 CC especially T-cell peptide epitopes with strong anti-tumour and anti-viral
 CC immune responses. Peptides AAW39572-W39585 are derived from the human
 CC Influenza M virus and are used in an assay to monitor the ability to bind
 CC to the human MHC Class I allele HLA-A2.1
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KTR 5
 |||

Db 7 KTR 9

RESULT 58

AAW14038

ID AAW14038 standard; peptide; 11 AA.

XX

AC AAW14038;

XX

DT 27-MAY-1997 (first entry)

XX

DE Anti-parasitic peptide #22.

XX

KW Anti-parasitic agent; cytotoxic; parasite.

XX

OS Synthetic.

XX

PN JP09040578-A.

XX

PD 10-FEB-1997.

XX

PF 31-JUL-1995; 95JP-00195218.

XX

PR 31-JUL-1995; 95JP-00195218.

XX

PA (MORG) MORINAGA MILK IND CO LTD.

XX

DR WPI; 1997-175617/16.

XX

PT Anti-parasite agent - shows no cytotoxicity to normal cells.

XX

PS Claim 1; Page 10; 11pp; Japanese.

XX

CC AAW14017-W14044 represent peptide sequence used in the anti-parasitic
CC agent of the invention. The anti-parasitic agent contains one of these
CC sequences, or a mixture of at least two of them (or derivatives, or salts
CC of these sequences) as the active component. The agent is an anti-
CC parasitic and has low side effects and shows no cytotoxicity to normal
CC cells. The agent is also stable in aqueous solution

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KTR 5

|||

Db 1 KTR 3

RESULT 59

AAW16616

ID AAW16616 standard; peptide; 11 AA.

XX

AC AAW16616;

XX

DT 19-DEC-1997 (first entry)
 XX
 DE Phosphoinositide-3 kinase p110alpha conserved motif.
 XX
 KW Phosphoinositide 3 kinase; PI-3 kinase; wortmannin.
 XX
 OS Synthetic.
 XX
 PN WO9715658-A1.
 XX
 PD 01-MAY-1997.
 XX
 PF 28-OCT-1996; 96WO-GB002614.
 XX
 PR 26-OCT-1995; 95GB-00021987.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Wymann MP, Bulgarelli-Vela G, Panayotou G, Vanhaesebroeck B;
 PI Zvelebil MJ, Waterfield MD;
 XX
 DR WPI; 1997-259013/23.
 XX
 PT Phospho:inositide 3 kinase wortmannin interaction site - to identify and
 PT design ligands which regulate phospho:inositide 3 kinase activity.
 XX
 PS Disclosure; Page 32; 71pp; English.
 XX
 CC A novel interaction site has been discovered on phosphoinositide 3 (PI-3)
 CC kinase, or a homologue or analogue. The interaction site modulates the
 CC activity of PI-3 kinase when exposed to a modulator, and has a molecular
 CC shape adapted to interact with at least a part of the modulator so as to
 CC modulate PI-3 kinase activity. The present sequence represents a
 CC conserved motif (resembling K(X)nKXKK where n=3-7) in PI-3 kinase
 CC p110alpha, that was found to bind phosphatidylinositol in gelsolin and so
 CC might constitute a binding site for the 4,5-phosphates of the lipid. The
 CC activity of PI-3 kinase can be regulated by altering, e.g. substituting a
 CC different amino acid or deleting any of the features of the site. The
 CC site may be used to identify or design novel ligands which regulate the
 CC activity of PI-3 kinase by generating a molecular model of the wortmannin
 CC inhibition site of PI-3 kinase, identifying or designing ligands which
 CC interact with at least part of the site and optionally contacting the
 CC putative ligand with PI-3 kinase and monitoring PI-3 kinase activity
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RER 7
 |||
 Db 9 RER 11

RESULT 60
 AAW10140

ID AAW10140 standard; peptide; 11 AA.
XX
AC AAW10140;
XX
DT 25-MAR-2003 (revised)
DT 02-OCT-1997 (first entry)
XX
DE Hepatitis C virus peptide antigen IIA.
XX
KW Antibody; HCV; immunoassay; vaccine; mimic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "H or a linker arm by which the peptide can be
FT attached to a carrier or solid phase comprising at least
FT one amino acid and as many as 60, most frequently 1-20
FT amino acids, such as Cys, Lys, Tyr, Glu or Asp, or
FT chemical groups such as biotin or thioglycolic acid; can
FT be modified by acetylation"
FT Modified-site 11
FT /note= "A bond or a linker arm by which the peptide can
FT be attached to a carrier or solid phase comprising at
FT least one amino acid and as many as 60 amino acids, most
FT frequently 1-10 amino acids, such as Cys, Lys, Tyr, Asp,
FT or chemical groups such as biotin or thioglycolic acid;
FT and attached on to that is NH2, OH or a linkage involving
FT either of these two groups"
XX
PN EP754704-A2.
XX
PD 22-JAN-1997.
XX
PF 14-DEC-1990; 96EP-00201157.
XX
PR 14-DEC-1990; 90EP-00124241.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Deleys RJ, Pollet D, Maertens G, Van Heuverswyn H;
XX
DR WPI; 1997-089256/09.
XX
PT Hepatitis C virus peptide mimics - for use in immunoassays, vaccines,
PT etc.
XX
PS Claim 2; Page 38; 65pp; English.
XX
CC The present sequence represents a novel synthetic Hepatitis C virus (HCV)
CC antigen IIA for the detection of antibodies. The peptide contains
CC modifications at the N- and C-terminal (see features table) with the
CC condition that if the modification represents an amino acid(s), that they
CC are different from any naturally occurring HCV flanking regions. The
CC peptide represents an HCV peptide mimic and may be used as an immunoassay
CC reagent for detecting antibodies to HCV; for incorporation into vaccines
CC against HCV; and for raising antibodies against HCV. (Updated on 25-MAR-

CC 2003 to correct PF field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKT 4

|||

Db 2 RKT 4

RESULT 61

AAW26152

ID AAW26152 standard; peptide; 11 AA.

XX

AC AAW26152;

XX

DT 24-NOV-1997 (first entry)

XX

DE Lactoferrin derivative #21.

XX

KW Lactoferrin; lactoferrin hydrolysate; derivative; neovascular disease;

KW ophthalmic disease; chronic rheumatism; abnormal capillary vessel;

KW psoriasis; therapy.

XX

OS Synthetic.

XX

PN JP09194388-A.

XX

PD 29-JUL-1997.

XX

PF 22-JAN-1996; 96JP-00008722.

XX

PR 22-JAN-1996; 96JP-00008722.

XX

PA (MORG) MORINAGA MILK IND CO LTD.

XX

DR WPI; 1997-431405/40.

XX

PT Peptide derived from lactoferrin or lactoferrin hydrolysate - for

PT treatment of neovascular diseases.

XX

PS Claim 3; Page 9; 11pp; Japanese.

XX

CC AAW26132-W26157 represent the peptide derivatives of the invention. These

CC sequences are derivatives of lactoferrin or lactoferrin hydrolysate. The

CC derivatives are used in an agent for the treatment of neovascular

CC diseases. The diseases that the peptides can be used to treat include

CC ophthalmic diseases, chronic rheumatism, psoriasis and abnormal capillary

CC vessels

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KTR 5
 | | |
Db 1 KTR 3

RESULT 62

AAW70312

ID AAW70312 standard; peptide; 11 AA.

XX

AC AAW70312;

XX

DT 06-NOV-1998 (first entry)

XX

DE Thrombus formation inhibitory peptide derivative 18.

XX

KW Polyethyleneglycol; PEG; thrombus; side effect; inhibitory peptide.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "attached by an acyl or polyethyleneglycol (PEG)
FT group"

FT Modified-site 11

FT /note= "attached by an amino, acyl, polyethyleneglycol
FT (PEG) or beta-alanine-PEG group"

XX

PN JP10182479-A.

XX

PD 07-JUL-1998.

XX

PF 24-DEC-1996; 96JP-00343590.

XX

PR 24-DEC-1996; 96JP-00343590.

XX

PA (MORG) MORINAGA MILK IND CO LTD.

XX

DR WPI; 1998-433772/37.

XX

PT Drug comprises peptide derivative used to inhibit thrombus formation -
PT optionally combined with and/or adsorbed onto carrier, has low side
PT effects.

XX

PS Disclosure; Page 12; 14pp; Japanese.

XX

CC The invention provides a drug composition comprising of a peptide
CC derivative of the formula (A) R1X, (B) XR2 or (C) R1XR2; where R1 = acyl
CC or polyethyleneglycol (PEG); R2 = amino, acyl, PEG or beta-alanine-PEG; X
CC = peptide sequence of 3-47 D or L amino acids such as the present
CC sequence. The drug is claimed to inhibit thrombus formation with low side
CC effect

XX

SQ Sequence 11 AA;

Query Match

27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KTR 5
|||
Db 1 KTR 3

RESULT 63

AAW69270

ID AAW69270 standard; peptide; 11 AA.

XX

AC AAW69270;

XX

DT 29-OCT-1998 (first entry)

XX

DE Haemagglutinin heavy chain (HA1) fragment.

XX

KW Acryloylated peptide polymer; immune response; peptide epitope;

KW synthetic vaccine; enzymatically cleavable site.

XX

OS Influenza virus.

XX

FH Key Location/Qualifiers

FT Misc-difference 1

FT /note= "linked to acryloylated peptide polymer"

XX

PN WO9834968-A1.

XX

PD 13-AUG-1998.

XX

PF 10-FEB-1998; 98WO-AU000076.

XX

PR 11-FEB-1997; 97AU-00005071.

PR 03-OCT-1997; 97CA-02217321.

XX

PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.

PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

PA (UYME) UNIV MELBOURNE.

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

PA (CSLC-) CSL LTD.

XX

PI Jackson DC, Obrien-Simpson NM, Brown LE, Zeng W, Ede NJ;

PI Brandt ER, Good MF;

XX

DR WPI; 1998-447177/38.

XX

PT Acryloylated peptide polymers - useful for synthetic vaccine technology,
PT for raising an immune response to peptide epitope and as diagnostic tool.

XX

PS Example 1; Page 20; 77pp; English.

XX

CC This sequence represents a fragment of the heavy chain (HA1) of the
CC haemagglutinin of influenza virus. This sequence was used to test the
CC acryloylated peptide polymer of the invention. The peptide polymers are
CC used to raise an immune response to a peptide epitope (such as this
CC sequence), and also as diagnostic tools. Polymers (molecular wt. >600

CC kDa.) can be prepared with virtually any number of the same or different
CC epitopes by a method that allows purification of the individual
CC determinants, avoids errors inherent in long sequential syntheses in
CC which protected peptide fragments are not used, thus avoiding solubility
CC and purification problems. Multiple copies of many different peptide
CC epitopes may be incorporated into a single polymeric structure to allow
CC utilisation of the range of T cell epitopes required for outbred
CC populations in conjunction with epitopes representing different
CC pathogenic serodemes, thus making them a significant advance in synthetic
CC vaccine technology

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ERK 8
|||
Db 7 ERK 9

RESULT 64

AAY20426

ID AAY20426 standard; protein; 11 AA.

XX

AC AAY20426;

XX

DT 22-JUL-1999 (first entry)

XX

DE Human microtubule associated protein 2 mutant fragment 122.

XX

KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW frameshift mutation; age-related disease; neurodegenerative disorder;
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
KW high mobility group protein-C; neuroendocrine specific protein A.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9845322-A2.

XX

PD 15-OCT-1998.

XX

PF 02-APR-1998; 98WO-IB000705.

XX

PR 10-APR-1997; 97US-0043163P.

XX

PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.

PA (UYRO-) UNIV ROTTERDAM ERASMUS.

PA (UYUT-) RIJKSUNIV UTRECHT.

XX
 PI Van Leeuwen FW, Grosveld FG, Burbach JPH;
 XX
 DR WPI; 1998-609901/51.
 DR N-PSDB; AAX75757.
 XX
 PT Diagnosing disease by detecting frameshift mutations in RNA or
 PT corresponding protein mutations - used to diagnose cancer and
 PT neurological diseases, particularly Alzheimer's disease, and also for
 PT treatment and prevention with specific ribozymes or wild-type RNA.
 XX
 PS Disclosure; Fig 6; 258pp; English.
 XX
 CC This invention describes a novel method for the diagnosis of a disease
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age-related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC used of neuronal system RNA molecules, specifically proteins including
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
 CC protein-C (HMGP-C) and neuroendocrine specific protein A
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKS 9
 |||
 Db 7 RKS 9

RESULT 65
 AAW78553
 ID AAW78553 standard; peptide; 11 AA.
 XX
 AC AAW78553;
 XX
 DT 04-NOV-1998 (first entry)
 XX
 DE SH2 domain binding inhibiting peptide SEQ ID NO:33.
 XX
 KW SH2 domain; binding; inhibition; interaction; site specific;
 KW signal transduction; protein tyrosine kinase; phosphotyrosine;
 KW growth factor receptor; oncogene; cellular growth; cell proliferation;
 KW metabolic control; diabetes; PTK; proto-oncogene; insulin receptor.

XX
 OS Synthetic.
 XX
 PN US5801149-A.
 XX
 PD 01-SEP-1998.
 XX
 PF 21-MAR-1995; 95US-00408604.
 XX
 PR 19-JUN-1991; 91US-00722359.
 PR 09-OCT-1992; 92US-00959949.
 PR 08-OCT-1993; 93US-00134558.
 XX
 PA (JOSL-) JOSLIN DIABETES CENT INC.
 XX
 PI Shoelson S;
 XX
 DR WPI; 1998-494822/42.
 XX
 PT Inhibiting site-specific SH2 domain interaction - with peptide containing
 PT phosphotyrosine or phosphotyrosine mimic.
 XX
 PS Disclosure; Col 43; 70pp; English.
 XX
 CC A method has been developed of inhibiting a site-specific interaction
 CC between a first molecule having an SH2 domain and a second molecule that
 CC interacts with the SH2 domain. The method comprises contacting the first
 CC molecule with a 4- to 30-mer peptide containing a sequence of formula: R1
 CC -Met-R3-Met (I), where R1 = phosphotyrosine (pTyr) or a phosphotyrosine
 CC analogue having a hydrolysis-resistant phosphorous moiety, and R3 = any
 CC amino acid. AAW78501 to AAW78523 represent specifically claimed examples
 CC of the peptides described. The peptides are useful for modulating both
 CC cellular growth to control unwanted cell proliferation in e.g. selected
 CC malignancies and for metabolic control in e.g. diabetes, by inhibiting
 CC signal transduction molecules such as protein tyrosine kinases (PTKs)
 CC which include growth factor receptors, proto-oncogene and oncogene
 CC products and the insulin receptor. The peptides are also useful for
 CC treating and for studying the enzymatic mechanisms of PTPase activity and
 CC the metabolic and biochemical roles of PTPases. AAW78524 to AAW78702
 CC represent other peptides given in the present invention, but which are
 CC not specifically claimed
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SKD 11
 |||
 Db 8 SKD 10

RESULT 66
 AAW78592
 ID AAW78592 standard; peptide; 11 AA.
 XX

AC AAW78592;
 XX
 DT 04-NOV-1998 (first entry)
 XX
 DE SH2 domain binding inhibiting peptide SEQ ID NO:79.
 XX
 KW SH2 domain; binding; inhibition; interaction; site specific;
 KW signal transduction; protein tyrosine kinase; phosphotyrosine;
 KW growth factor receptor; oncogene; cellular growth; cell proliferation;
 KW metabolic control; diabetes; PTK; proto-oncogene; insulin receptor.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 4
 FT /note= "unspecified"
 XX
 PN US5801149-A.
 XX
 PD 01-SEP-1998.
 XX
 PF 21-MAR-1995; 95US-00408604.
 XX
 PR 19-JUN-1991; 91US-00722359.
 PR 09-OCT-1992; 92US-00959949.
 PR 08-OCT-1993; 93US-00134558.
 XX
 PA (JOSL-) JOSLIN DIABETES CENT INC.
 XX
 PI Shoelson S;
 XX
 DR WPI; 1998-494822/42.
 XX
 PT Inhibiting site-specific SH2 domain interaction - with peptide containing
 PT phosphotyrosine or phosphotyrosine mimic.
 XX
 PS Disclosure; Col 61; 70pp; English.
 XX
 CC A method has been developed of inhibiting a site-specific interaction
 CC between a first molecule having an SH2 domain and a second molecule that
 CC interacts with the SH2 domain. The method comprises contacting the first
 CC molecule with a 4- to 30-mer peptide containing a sequence of formula: R1
 CC -Met-R3-Met (I), where R1 = phosphotyrosine (pTyr) or a phosphotyrosine
 CC analogue having a hydrolysis-resistant phosphorous moiety, and R3 = any
 CC amino acid. AAW78501 to AAW78523 represent specifically claimed examples
 CC of the peptides described. The peptides are useful for modulating both
 CC cellular growth to control unwanted cell proliferation in e.g. selected
 CC malignancies and for metabolic control in e.g. diabetes, by inhibiting
 CC signal transduction molecules such as protein tyrosine kinases (PTKs)
 CC which include growth factor receptors, proto-oncogene and oncogene
 CC products and the insulin receptor. The peptides are also useful for
 CC treating and for studying the enzymatic mechanisms of PTPase activity and
 CC the metabolic and biochemical roles of PTPases. AAW78524 to AAW78702
 CC represent other peptides given in the present invention, but which are
 CC not specifically claimed
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SKD 11
|||
Db 8 SKD 10

RESULT 67

AAW41292

ID AAW41292 standard; peptide; 11 AA.

XX

AC AAW41292;

XX

DT 20-MAY-1998 (first entry)

XX

DE Apoptosis inducer peptide.

XX

KW Apoptosis inducer; hydrolysed lactoferrin.

XX

OS Synthetic.

XX

PN JP10045618-A.

XX

PD 17-FEB-1998.

XX

PF 26-JUL-1996; 96JP-00198196.

XX

PR 26-JUL-1996; 96JP-00198196.

XX

PA (MORG) MORINAGA MILK IND CO LTD.

XX

DR WPI; 1998-189187/17.

XX

PT New inducer(s) of apoptosis - comprise active parts of peptide(s) derived
PT from hydrolysis of lactoferrin.

XX

PS Claim 3; Page 10; 11pp; Japanese.

XX

CC This sequence represents an apoptosis inducer peptide of the invention.

CC The apoptosis inducers comprising active parts of peptides derived from

CC hydrolysed lactoferrin. The peptides can be used to prepare therapeutic

CC compositions in the form of tablets, capsules or injections. The inducers

CC are safe and do not cause adverse reactions

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KTR 5
|||
Db 1 KTR 3

RESULT 68

AAW61162

ID AAW61162 standard; peptide; 11 AA.

XX

AC AAW61162;

XX

DT 26-OCT-1998 (first entry)

XX

DE IgE derived oligopeptide 1.

XX

KW IgE Fc epsilon receptor; Cysteine; disulphide bond; loop structure;

KW anti-allergy treatment; anaphylatic immune response; antibody;

KW Type I hypersensitivity; hay fever; asthma.

XX

OS Homo sapiens.

XX

PN WO9824808-A2.

XX

PD 11-JUN-1998.

XX

PF 05-DEC-1997; 97WO-US022348.

XX

PR 06-DEC-1996; 96US-0031991P.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Padlan EA, Birgit AH;

XX

DR WPI; 1998-333254/29.

XX

PT Oligopeptide interacting with human IgE Fc epsilon receptor - useful in

PT anti-allergy treatment as competitors of human IgE for Fc epsilon

PT receptor to block development of Type I hypersensitivity.

XX

PS Claim 1; Page 3; 45pp; English.

XX

CC The sequences AAW61162-W61166 are IgE derived oligopeptides which
CC interact with the human IgE Fc epsilon receptor. This particular
CC oligopeptide is the core minimal region of IgE required for interaction
CC with these Fc epsilon receptors and can thus bind both high and low
CC affinity receptors. The peptide was derived from a region of the epsilon
CC heavy chain of IgE, and can therefore mimic and block human IgE binding
CC to the Fc receptors. This sequence was used as the core sequence in the
CC other oligopeptides that were derived, they varied in length and at their
CC N and C terminal end. The IgE protein forms a loop structure naturally,
CC thus the addition of Cysteine residues at both ends of this sequence
CC enables disulphide bonds to form which results in a loop structure. These
CC oligopeptides are small and are thus easy to synthesise and deliver, they
CC are stable, highly active in anti-allergy treatment and lastly are less
CC likely to trigger an adverse anaphylatic immune response. The
CC oligopeptides can be used as competitors of human IgE for the Fc epsilon
CC receptor in anti-allergy treatment. Human IgE mediates Type I
CC hypersensitivity, an allergic response producing symptoms such as hay
CC fever and asthma. Thus the oligopeptides can be used to block the
CC development of type I hypersensitivity

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKS 9
|||
Db 9 RKS 11

RESULT 69

AAW53227

ID AAW53227 standard; peptide; 11 AA.

XX

AC AAW53227;

XX

DT 09-JUL-1998 (first entry)

XX

DE Lactoferrin hydrolysate peptide SEQ ID NO:27.

XX

KW Oral agent; cancer; metastasis; iron-free saturated lactoferrin;

KW hydrolysate; food; beverage.

XX

OS Synthetic.

XX

PN WO9806424-A1.

XX

PD 19-FEB-1998.

XX

PF 01-AUG-1997; 97WO-JP002685.

XX

PR 15-AUG-1996; 96JP-00233652.

XX

PA (MORG) MORINAGA MILK IND CO LTD.

XX

PI Tsuda H, Iigo M, Tomita M, Shimamura S, Takatsu Z, Sekine K;

XX

DR WPI; 1998-159285/14.

XX

PT Oral agent for the control of cancer metastasis - comprising iron-free
PT saturated lactoferrin, or its hydrolysate or peptide derivative.

XX

PS Claim 4; Page 37; 46pp; Japanese.

XX

CC The present sequence represents a specifically claimed peptide of the
CC present invention. The present invention describes an oral agent for the
CC control of cancer metastasis. The oral agent comprises one or more of
CC iron-free saturated lactoferrin, or a lactoferrin hydrolysate or salt, or
CC peptide from lactoferrin hydrolysate, or a salt or derivative of these
CC peptide. Also described is a foodstuff or beverage containing the agent.
CC The agent is used to control metastasis and lactoferrin or its
CC hydrolysate or salt, is administered at a dosage of 3-3200 mg/kg/day and
CC the peptide is administered at a dosage of 0.2-320 mg/kg/day. The
CC products are simple to take, can be given for a long time, and have few
CC side effects

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KTR 5
|||
Db 1 KTR 3

RESULT 70

AAY30697

ID AAY30697 standard; peptide; 11 AA.

XX

AC AAY30697;

XX

DT 17-NOV-1999 (first entry)

XX

DE Apo-B100 derived peptide showing a proteoglycan receptor mutation.

XX

KW Apo-B100; proteoglycan receptor mutation; atherosclerosis;

KW low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9946598-A1.

XX

PD 16-SEP-1999.

XX

PF 05-MAR-1999; 99WO-US004805.

XX

PR 10-MAR-1998; 98US-0077618P.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Innerarity TL, Boren JOS;

XX

DR WPI; 1999-551509/46.

XX

PT Identifying compounds which affect binding of low density lipoprotein

PT with proteoglycan, used for, e.g. obtaining compounds for reducing

PT atherosclerosis.

XX

PS Claim 17; Page 57; 70pp; English.

XX

CC AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan
CC receptor mutations. They were created to identify compounds which
CC modulate atherosclerosis. The peptides are derived from amino acids 3358
CC to 3367 of apoB100. The method comprises detecting compounds which affect
CC low density lipoprotein (LDL) binding with proteoglycan (PG). The method
CC can be used for identifying compounds which disrupt LDL-PG binding
CC without inhibiting LDL receptor binding. Such compounds can be used to
CC reduce or prevent the formation of atherosclerotic lesions and prevent
CC atherosclerosis. The transgenic non-human animals and mammals which
CC express human apo-B100 can be used as an in vivo model system for the

CC study of atherosclerosis, and in vivo assay methods for identifying
CC compounds which modulate atherosclerosis and/or LDL-PG binding. They can
CC also be used to identify compounds which result in an increase in
CC atherosclerotic regions. Thus the assays may be used to determine whether
CC a particular food or drug composition tends to stimulate or inhibit the
CC formation of atherosclerotic lesions. The polynucleotides can also be
CC used in gene therapy for preventing or reducing the severity of
CC atherosclerosis in an animal or mammal

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TRE 6

|||

Db 4 TRE 6

RESULT 71

AAY33387

ID AAY33387 standard; peptide; 11 AA.

XX

AC AAY33387;

XX

DT 01-DEC-1999 (first entry)

XX

DE Zinc finger clone zfHHA(Y) peptide fragment.

XX

KW Zinc finger; DNA binding; Cys2-His2 class; 5-methylcytosine; meC;

KW diagnostic; detection; chimera.

XX

OS Unidentified.

XX

PN WO9947656-A2.

XX

PD 23-SEP-1999.

XX

PF 17-MAR-1999; 99WO-GB0000816.

XX

PR 17-MAR-1998; 98GB-00005576.

PR 31-MAR-1998; 98GB-00006895.

PR 03-APR-1998; 98GB-00007246.

XX

PA (MEDI-) MEDICAL RES COUNCIL.

XX

PI Choo Y, Isalan M;

XX

DR WPI; 1999-562106/47.

XX

PT New zinc finger polypeptides that bind DNA containing modified bases,

PT used as diagnostic and research reagents and for regulating gene

PT transcription.

XX

PS Disclosure; Fig 3; 56pp; English.

XX

CC This invention describes a novel zinc finger (ZF) polypeptide (I) that
 CC binds to a target DNA sequence (II) containing a modified base but not to
 CC an otherwise identical sequence containing the equivalent unmodified
 CC base. The invention also describes methods for preparing a DNA-binding
 CC polypeptide of the Cys2-His2 ZF class, able to recognize sequences
 CC containing a 5-methylcytosine (meC) residue. (I) are used as diagnostic
 CC reagents (for detecting modified nucleic acids in complex mixtures,
 CC including differentiation of single-base modifications), in research and
 CC to produce chimeras, e.g. by fusion to a catalytic domain of a
 CC restriction enzyme (the product can then cleave only modified DNA), or to
 CC a DNA cleavage or activating domain (to give products that can regulate
 CC gene transcription, by sequence-specific cleavage or activation,
 CC dependent on presence of a modified base). (I) recognize modified bases
 CC in preference to unmodified ones, in a sequence-dependent manner, so have
 CC extremely high specificity. This sequence represents a zinc finger clone
 CC peptide fragment described in the method of the invention
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KTR 5
 |||
 Db 1 KTR 3

RESULT 72

AA03092

ID AA03092 standard; peptide; 11 AA.

XX

AC AA03092;

XX

DT 08-JUN-1999 (first entry)

XX

DE New nociceptin analogue #74 from W09903880.

XX

KW Nociceptin; vasomotor disorder; menopausal hot flush; opioid antagonist;
 KW hyperalgesia; neuroendocrine secretion; stress; locomotor activity;
 KW anxiety; instinctive behaviour; learning disorder; memory disorder;
 KW attention disorder; sensory perception disorder.

XX

OS Synthetic.

XX

FH	Key	Location/Qualifiers
FT	Modified-site	6. .10
FT		/note= "the side chains of residues 6 and 10 are
FT		condensed via a Gly residue to form a lactam bridge
FT		between these two positions"
FT	Modified-site	10
FT		/label= Orn
FT		/note= "ornithine residue"
FT	Modified-site	11
FT		/note= "C-terminal amide"

XX

PN W09903880-A1.

XX
 PD 28-JAN-1999.
 XX
 PF 13-JUL-1998; 98WO-DK000326.
 XX
 PR 15-JUL-1997; 97DK-00000867.
 PR 17-JUL-1997; 97US-0052862P.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Thogersen H, Madsen K, Olsen UB, Johansen NL, Scheideler M;
 XX
 DR WPI; 1999-132156/11.
 XX
 PT New derivatives of nociceptin for treating vasomotor disorders -
 PT specifically hot flushes in menopausal women.
 XX
 PS Claim 70; Page 61; 69pp; English.
 XX
 CC This sequence is a specifically claimed example of new nociceptin
 CC analogue peptides which have the generic formula (X)_n-A1-A2-A3-A4-A5- A6-
 CC A7-A8-A9-A10-A11-A12-A13-A14-A15-A16-A17-(Y)_m-A18, in which: A1 is
 CC absent, a small or lipophilic amino acid, or phenylpropionic acid,
 CC optionally acylated; A2 = aromatic, lipophilic or small amino acid,
 CC optionally acylated if A1 is absent; A3, A6 and A7 = small, lipophilic or
 CC polar amino acids; A2-A3 may alternatively be 5-amino-pentanoic, N-
 CC methylanthranilic, 4-aminocyclohexane carboxylic or 3-aminomethyl-
 CC benzoic acid; A4 = small, polar or aromatic amino acid; alternatively A3-
 CC A4 = N-methylanthranilic acid; A5, A9, A10 and A11 = lipophilic or polar
 CC amino acids; A8 = polar amino acids or D- or L-Ala; A12, A13, A14 and A15
 CC = polar or lipophilic amino acids or may be absent; A16 and A17= small or
 CC polar amino acids or may be absent; A18 = hydroxy or amino; X and Y =
 CC polar, lipophilic, aromatic or small amino acids; n + m = 0-82; and two
 CC or more of A1-A17, X and Y may be cyclisation amino acids, forming one or
 CC more bridges (disulphide, lactam or Gly-lactam); provided that the
 CC peptide has (a) at least two amino acids modifications relative to the
 CC nociceptin sequence or (b) an unnatural amino acid at position A1. These
 CC peptides are useful for treatment and prevention of vasomotor disorders,
 CC specifically hot flushes in menopausal women. They can also be used for
 CC antagonising the physiological effects of opioids and for treating
 CC diseases related to hyperalgesia, neuroendocrine secretion, stress,
 CC locomotor activity, anxiety, instinctive behaviour, and decrease in
 CC learning, memory, curiosity, attention and/or sensory perception
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
 |||
 Db 7 ARK 9

RESULT 73
 AAY47022

ID AAY47022 standard; peptide; 11 AA.
XX
AC AAY47022;
XX
DT 01-DEC-1999 (first entry)
XX
DE Immunogenic peptide having a human leukocyte antigen binding motif #1633.
XX
KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW immune response; T cell activation; major histocompatibility complex;
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW vaccine; immunisation.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9945954-A1.
XX
PD 16-SEP-1999.
XX
PF 13-MAR-1998; 98WO-US005039.
XX
PR 13-MAR-1998; 98WO-US005039.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX
DR WPI; 1999-551214/46.
XX
PT New immunogenic peptides with HLA binding motif, useful in treatment and
PT diagnosis of cancers and viral diseases.
XX
PS Claim 1; Page 91; 150pp; English.
XX
CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
CC having a human major histocompatibility complex (MHC) Class I (also known
CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
CC (CTLs) which destroy antigen-bearing cells are normally induced by an
CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
CC than the intact foreign antigen itself, and are particularly important in
CC tumour rejection and in fighting viral infections. The peptides are
CC therefore useful therapeutically to treat or prevent viral infections and
CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
CC elicit an immune response in individuals susceptible or otherwise at risk
CC of viral infection or cancer, or used to treat chronic or acute
CC conditions. They are also useful diagnostically, and can be used to
CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
CC patient. The polynucleotides encoding the immunogenic peptides are also
CC useful therapeutically and for immunisation as above
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KTR 5
|||
Db 1 KTR 3

RESULT 74

AAAY07983

ID AAY07983 standard; protein; 11 AA.

XX

AC AAY07983;

XX

DT 06-JUL-1999 (first entry)

XX

DE Human secreted protein fragment #3 encoded from gene 38.

XX

KW Human; secreted protein; treatment; prevention; protein therapy; AIDS;

KW gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder;

KW developmental abnormality; fetal deficiency; blood disorder; leukemia;

KW immune system disease; autoimmune disease; hepatic disease; lymphoma;

KW renal disease; inflammation; allergy; Alzheimer's disease; schizophrenia;

KW cognitive disorder; prostate disease; skeletal; cardiac; muscle disorder;

KW pulmonary disorder; transplant rejection; osteoclast; osteoporosis;

KW arthritis; malignancy; digestive; endocrine; infection.

XX

OS Homo sapiens.

XX

PN W09918208-A1.

XX

PD 15-APR-1999.

XX

PF 01-OCT-1998; 98WO-US020775.

XX

PR 02-OCT-1997; 97US-0060833P.

PR 02-OCT-1997; 97US-0060836P.

PR 02-OCT-1997; 97US-0060837P.

PR 02-OCT-1997; 97US-0060838P.

PR 02-OCT-1997; 97US-0060839P.

PR 02-OCT-1997; 97US-0060843P.

PR 02-OCT-1997; 97US-0060862P.

PR 02-OCT-1997; 97US-0060866P.

PR 02-OCT-1997; 97US-0060874P.

PR 02-OCT-1997; 97US-0060880P.

PR 02-OCT-1997; 97US-0060884P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Duan DR, Florence KA, Rosen CA, Ruben SM, Greene JM, Young P;

PI Ferrie AM, Yu G, Janat F, Ni J, Carter KC, Endress GA, Feng P;

PI Lafleur DW, Shi Y;

XX

DR WPI; 1999-264022/22.

XX
PT New isolated human genes and the secreted polypeptides they encode.
XX
PS Disclosure; Page 342; 368pp; English.
XX
CC This invention describes novel isolated human genes and the secreted
CC proteins they encode. The products of the invention are useful for
CC preventing, treating or ameliorating medical conditions, e.g. by protein
CC or gene therapy. Also pathological conditions can be diagnosed by
CC determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 101 polynucleotides, based on
CC which tissues they are most highly expressed in, and include developing
CC products for the diagnosis or treatment of cancer, tumours,
CC neurodegenerative disorders, developmental abnormalities and fetal
CC deficiencies, blood disorders, leukemias, diseases of the immune system,
CC autoimmune diseases, hepatic and renal disease, lymphomas, inflammation,
CC allergies, Alzheimer's and cognitive disorders, schizophrenia, prostate
CC disease, skeletal or cardiac muscle disorders, pulmonary disorders,
CC transplant rejection, disorders involving osteoclasts such as
CC osteoporosis, arthritis or malignancies, digestive/endocrine disorders,
CC infections and AIDS. The human secreted proteins of the invention are
CC represented in AAY07852-Y07993 and the encoding nucleic acids are
CC represented in AAX37451-X37552
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ERK 8
|||
Db 8 ERK 10

RESULT 75
AAW67680
ID AAW67680 standard; peptide; 11 AA.
XX
AC AAW67680;
XX
DT 16-MAR-1999 (first entry)
XX
DE LXXLL signature motif #13 from protein RIP140.
XX
KW Nuclear protein; signature motif; receptor protein; inflammation; cancer;
KW interaction; inhibitor; inhibition; transcription factor; ligand.
XX
OS Homo sapiens.
XX
PN WO9849561-A1.
XX
PD 05-NOV-1998.
XX
PF 28-APR-1998; 98WO-GB001238.
XX

PR 30-APR-1997; 97GB-00008676.

XX

PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.

XX

PI Heery DM, Parker MG;

XX

DR WPI; 1999-034672/03.

XX

PT Identification of inhibitors of nuclear protein/nuclear receptor
PT interaction - useful for, e.g. treatment of disease mediated through the
PT interaction such as inflammation and cancer.

XX

PS Example 2; Fig 3A; 60pp; English.

XX

CC This sequence represents an LXXLL nuclear protein signature motif found
CC in the 140 kD receptor interacting protein (RIP140) from nuclei. This
CC peptide corresponds to amino acids 184-194 of RIP140. The invention
CC relates to the identification of inhibitor compounds capable of reducing
CC the interaction between a region on a nuclear protein (R1) and a region
CC on a nuclear receptor (R2), where: (i) R1 is a signature motif; (ii) R2
CC is the region capable of interacting with the nuclear protein by binding
CC the signature motif; (iii) the nuclear protein is a bridging factor
CC responsible for interaction between a liganded nuclear receptor and a
CC transcription initiation complex involved in gene expression regulation;
CC (iv) the nuclear receptor is a transcription factor; (v) the signature
CC motif is a short amino acid sequence which is the key structural element
CC of a nuclear protein which binds to a liganded nuclear receptor during
CC activation or repression of target genes. The inhibitors are expected to
CC be useful in the treatment of any disease mediated through any
CC interaction between a signature motif on a nuclear protein and a nuclear
CC receptor, for example inflammation and cancer

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KSK 10

|||

Db 8 KSK 10

Search completed: April 8, 2004, 15:40:01

Job time : 46.3077 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:08 ; Search time 11.3077 Seconds
(without alignments)
50.221 Million cell updates/sec

Title: US-09-787-443A-14
Perfect score: 11
Sequence: 1 ARKTRERKSKD 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8542

Minimum DB seq length: 11
Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query					Description
No.	Score	Match	Length	DB	ID		
1	4	36.4	11	3	US-08-746-160-51	Sequence 51, Appl	
2	4	36.4	11	3	US-08-810-324-46	Sequence 46, Appl	
3	4	36.4	11	3	US-08-679-006-16	Sequence 16, Appl	
4	4	36.4	11	4	US-09-576-824A-482	Sequence 482, App	
5	3	27.3	11	1	US-07-851-941-11	Sequence 11, Appl	
6	3	27.3	11	1	US-07-851-941-18	Sequence 18, Appl	
7	3	27.3	11	1	US-08-185-448-5	Sequence 5, Appli	
8	3	27.3	11	1	US-08-480-505-1	Sequence 1, Appli	
9	3	27.3	11	1	US-08-428-488-17	Sequence 17, Appl	
10	3	27.3	11	1	US-08-256-771-27	Sequence 27, Appl	
11	3	27.3	11	1	US-08-445-745-122	Sequence 122, App	

12	3	27.3	11	1	US-08-615-181-84	Sequence 84, Appl
13	3	27.3	11	1	US-08-191-338A-15	Sequence 15, Appl
14	3	27.3	11	1	US-08-408-604A-33	Sequence 33, Appl
15	3	27.3	11	1	US-08-408-604A-79	Sequence 79, Appl
16	3	27.3	11	1	US-08-633-760-37	Sequence 37, Appl
17	3	27.3	11	1	US-08-381-984-31	Sequence 31, Appl
18	3	27.3	11	2	US-08-737-085A-12	Sequence 12, Appl
19	3	27.3	11	2	US-07-737-371E-73	Sequence 73, Appl
20	3	27.3	11	2	US-08-466-975A-3	Sequence 3, Appli
21	3	27.3	11	2	US-08-391-671A-3	Sequence 3, Appli
22	3	27.3	11	2	US-08-747-137-63	Sequence 63, Appl
23	3	27.3	11	2	US-08-482-228-200	Sequence 200, App
24	3	27.3	11	2	US-08-751-767A-29	Sequence 29, Appl
25	3	27.3	11	2	US-09-115-209-74	Sequence 74, Appl
26	3	27.3	11	3	US-08-467-902A-3	Sequence 3, Appli
27	3	27.3	11	3	US-08-482-528-200	Sequence 200, App
28	3	27.3	11	3	US-09-246-258-12	Sequence 12, Appl
29	3	27.3	11	3	US-08-444-818-105	Sequence 105, App
30	3	27.3	11	3	US-08-392-542-4	Sequence 4, Appli
31	3	27.3	11	3	US-08-392-542-13	Sequence 13, Appl
32	3	27.3	11	3	US-08-602-999A-283	Sequence 283, App
33	3	27.3	11	3	US-08-652-877-73	Sequence 73, Appl
34	3	27.3	11	3	US-09-208-966-3	Sequence 3, Appli
35	3	27.3	11	3	US-08-647-405B-3	Sequence 3, Appli
36	3	27.3	11	3	US-08-647-405B-4	Sequence 4, Appli
37	3	27.3	11	3	US-08-647-405B-6	Sequence 6, Appli
38	3	27.3	11	3	US-09-177-249-212	Sequence 212, App
39	3	27.3	11	3	US-09-177-249-253	Sequence 253, App
40	3	27.3	11	3	US-08-476-515A-73	Sequence 73, Appl
41	3	27.3	11	3	US-08-894-327-4	Sequence 4, Appli
42	3	27.3	11	3	US-08-894-327-13	Sequence 13, Appl
43	3	27.3	11	3	US-09-532-106-12	Sequence 12, Appl
44	3	27.3	11	3	US-09-275-265-3	Sequence 3, Appli
45	3	27.3	11	4	US-08-456-466-100	Sequence 100, App
46	3	27.3	11	4	US-09-311-626B-30	Sequence 30, Appl
47	3	27.3	11	4	US-09-685-027-4	Sequence 4, Appli
48	3	27.3	11	4	US-09-685-027-13	Sequence 13, Appl
49	3	27.3	11	4	US-09-500-124-283	Sequence 283, App
50	3	27.3	11	4	US-08-255-208A-77	Sequence 77, Appl
51	3	27.3	11	4	US-09-839-666-12	Sequence 12, Appl
52	3	27.3	11	4	US-09-082-358B-64	Sequence 64, Appl
53	3	27.3	11	4	US-09-410-551B-57	Sequence 57, Appl
54	3	27.3	11	4	US-09-101-272G-39	Sequence 39, Appl
55	3	27.3	11	4	US-08-445-638-122	Sequence 122, App
56	3	27.3	11	4	US-09-941-611-3	Sequence 3, Appli
57	3	27.3	11	4	US-09-265-222-16	Sequence 16, Appl
58	3	27.3	11	4	US-09-535-852-1119	Sequence 1119, Ap
59	3	27.3	11	4	US-09-535-852-1159	Sequence 1159, Ap
60	3	27.3	11	4	US-09-775-052A-3	Sequence 3, Appli
61	3	27.3	11	4	US-09-790-497A-39	Sequence 39, Appl
62	3	27.3	11	4	US-09-576-824A-477	Sequence 477, App
63	3	27.3	11	4	US-09-576-824A-478	Sequence 478, App
64	3	27.3	11	4	US-09-576-824A-479	Sequence 479, App
65	3	27.3	11	4	US-09-576-824A-480	Sequence 480, App
66	3	27.3	11	4	US-09-576-824A-481	Sequence 481, App
67	3	27.3	11	4	US-09-576-824A-546	Sequence 546, App
68	3	27.3	11	4	US-09-576-824A-547	Sequence 547, App

69	3	27.3	11	4	US-09-576-824A-548	Sequence 548, App
70	3	27.3	11	4	US-09-576-824A-549	Sequence 549, App
71	3	27.3	11	5	PCT-US91-08328-13	Sequence 13, Appl
72	3	27.3	11	5	PCT-US91-08328-14	Sequence 14, Appl
73	3	27.3	11	5	PCT-US91-08328-16	Sequence 16, Appl
74	3	27.3	11	5	PCT-US91-08328-18	Sequence 18, Appl
75	3	27.3	11	5	PCT-US91-08328-20	Sequence 20, Appl
76	3	27.3	11	5	PCT-US92-09070-10	Sequence 10, Appl
77	3	27.3	11	5	PCT-US93-09626-33	Sequence 33, Appl
78	3	27.3	11	6	5187155-26	Patent No. 5187155
79	3	27.3	11	6	5190919-10	Patent No. 5190919
80	3	27.3	11	6	5223254-12	Patent No. 5223254
81	2	18.2	11	1	US-07-620-669-10	Sequence 10, Appl
82	2	18.2	11	1	US-07-620-669-11	Sequence 11, Appl
83	2	18.2	11	1	US-07-696-551B-10	Sequence 10, Appl
84	2	18.2	11	1	US-07-719-692A-10	Sequence 10, Appl
85	2	18.2	11	1	US-07-778-233B-26	Sequence 26, Appl
86	2	18.2	11	1	US-07-963-321-26	Sequence 26, Appl
87	2	18.2	11	1	US-07-838-264-3	Sequence 3, Appli
88	2	18.2	11	1	US-07-838-264-4	Sequence 4, Appli
89	2	18.2	11	1	US-08-049-871-6	Sequence 6, Appli
90	2	18.2	11	1	US-07-791-935B-13	Sequence 13, Appl
91	2	18.2	11	1	US-07-819-893-6	Sequence 6, Appli
92	2	18.2	11	1	US-07-803-624-10	Sequence 10, Appl
93	2	18.2	11	1	US-07-803-624-11	Sequence 11, Appl
94	2	18.2	11	1	US-07-998-361-10	Sequence 10, Appl
95	2	18.2	11	1	US-07-998-361-11	Sequence 11, Appl
96	2	18.2	11	1	US-08-029-333-21	Sequence 21, Appl
97	2	18.2	11	1	US-08-030-731A-20	Sequence 20, Appl
98	2	18.2	11	1	US-07-851-941-12	Sequence 12, Appl
99	2	18.2	11	1	US-07-851-941-13	Sequence 13, Appl
100	2	18.2	11	1	US-07-851-941-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-08-746-160-51

; Sequence 51, Application US/08746160

; Patent No. 6010876

; GENERAL INFORMATION:

; APPLICANT: Lehrer, Robert I.

; APPLICANT: Harwig, Sylvia L.

; APPLICANT: Zhao, Chengquan

; APPLICANT: Lee, In-Hee

; TITLE OF INVENTION: CLAVANINS

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 2000 Pennsylvania Avenue, NW, suite 5500

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20006-1888

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

```

;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/746,160
;      FILING DATE:  06-NOV-1996
;      CLASSIFICATION:  530
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  22000-20563.00
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;      TELEFAX:  202-822-0168
;      TELEX:
;      INFORMATION FOR SEQ ID NO:  51:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-746-160-51

```

```

Query Match          36.4%;  Score 4;  DB 3;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.9e+02;
Matches      4;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      6 ERKS 9
        ||||
Db      4 ERKS 7

```

```

RESULT 2
US-08-810-324-46
; Sequence 46, Application US/08810324C
; Patent No. 6040293
; GENERAL INFORMATION:
; APPLICANT: LEHRER, Robert I
; APPLICANT: ZHAO, Chengquan
; APPLICANT: LEE, In-Hee
; APPLICANT: HARWIG, Sylvia L.
; TITLE OF INVENTION: CLAVANINS
; FILE REFERENCE: 22000-20563.20
; CURRENT APPLICATION NUMBER: US/08/810,324C
; CURRENT FILING DATE: 1997-02-28
; EARLIER APPLICATION NUMBER: 08/746,160
; EARLIER FILING DATE: 1996-11-06
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Styela clava
US-08-810-324-46

```

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ERKS 9
||||
Db 4 ERKS 7

RESULT 3

US-08-679-006-16
; Sequence 16, Application US/08679006
; Patent No. 6150500
; GENERAL INFORMATION:
; APPLICANT: Salerno, John C.
; TITLE OF INVENTION: APPLICATIONS FOR REGULATORY REGION OF
; TITLE OF INVENTION: NOS ISOFORMS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,006
; FILING DATE: 12-JUL-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: JCS96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-679-006-16

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ERKS 9
||||

Db

3 ERKS 6

RESULT 4

US-09-576-824A-482

; Sequence 482, Application US/09576824A

; Patent No. 6667387

; GENERAL INFORMATION:

; APPLICANT: De Leys, Robert

; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING

; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN

; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF

; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY
IMPORTANT

; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS

; TITLE OF INVENTION: CONTAINING THEM

; FILE REFERENCE: 2752-11

; CURRENT APPLICATION NUMBER: US/09/576,824A

; CURRENT FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 08/723,425

; PRIOR FILING DATE: 1996-09-30

; PRIOR APPLICATION NUMBER: 09/146,028

; PRIOR FILING DATE: 1993-11-22

; PRIOR APPLICATION NUMBER: PCT/EP93/00517

; PRIOR FILING DATE: 1993-03-08

; PRIOR APPLICATION NUMBER: EP 92400598.6

; PRIOR FILING DATE: 1992-03-06

; NUMBER OF SEQ ID NOS: 600

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 482

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Hepatitis C virus

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: (1)

; OTHER INFORMATION: Xaa = modified site : when present, represents an

; OTHER INFORMATION: amino acid, amino group, or chemically modified

; OTHER INFORMATION: amino terminus

; NAME/KEY: VARIANT

; LOCATION: (11)

; OTHER INFORMATION: Xaa = modified site : when present, represents an

; OTHER INFORMATION: amino acid, OH-group, NH2-group, or a linkage

; OTHER INFORMATION: involv-ing these two groups

US-09-576-824A-482

Query Match 36.4%; Score 4; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARKT 4

||||

Db 1 ARKT 4

RESULT 5

US-07-851-941-11

; Sequence 11, Application US/07851941
; Patent No. 5428016
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptide and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/851,941
; FILING DATE: 19920313
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/851,941
; FILING DATE: March 13, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acid residues
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:

```

; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-851-941-11

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      3 KTR 5
        |||
Db      1 KTR 3

```

RESULT 6

US-07-851-941-18

```

; Sequence 18, Application US/07851941
; Patent No. 5428016
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptide and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/851,941
; FILING DATE: 19920313
; CLASSIFICATION: 530

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/851,941
; FILING DATE: March 13, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acid residues
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: modified site
; LOCATION: 11
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "Lys-NH2"
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-851-941-18

```

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KTR 5
|||
Db 1 KTR 3

RESULT 7

US-08-185-448-5

; Sequence 5, Application US/08185448

; Patent No. 5580747

; GENERAL INFORMATION:

; APPLICANT: SHULTZ, JOHN W.

; APPLICANT: WHITE, DOUGLAS H.

; TITLE OF INVENTION: NON-RADIOACTIVE KINASE,

; TITLE OF INVENTION: PHOSPHATASE AND PROTEASE ASSAY

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL

; STREET: 100 E. WISCONSIN AVENUE, SUITE 1100

; CITY: MILWAUKEE

; STATE: WISCONSIN

; COUNTRY: USA

; ZIP: 53202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version

; SOFTWARE: #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/185,448

; FILING DATE: 21-JAN-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/791,928

; FILING DATE: 12-NOV-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: SARA, CHARLES S

; REGISTRATION NUMBER: 30492

; REFERENCE/DOCKET NUMBER: F.3347-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (608) 255-2022

; TELEFAX: (608) 255-2182

; TELEX: 26832 ANDSTARK

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Binding-site

; LOCATION: 1

; OTHER INFORMATION: /label= LABEL

; OTHER INFORMATION: /note= "LOCATION OF LISSAMINE RHODAMINE
; OTHER INFORMATION: DETECTION TAG"
US-08-185-448-5

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKS 9
|||
Db 5 RKS 7

RESULT 8

US-08-480-505-1

; Sequence 1, Application US/08480505

; Patent No. 5601821

; GENERAL INFORMATION:

; APPLICANT: STANWORTH, DENIS R

; APPLICANT: LEWIN, IAN V

; APPLICANT: NAYYAR, SARITA

; APPLICANT: JONES, VALERIE

; TITLE OF INVENTION: IMMUNOACTIVE PEPTIDES AND ANTIBODIES AND

; TITLE OF INVENTION: THEIR USE IN ANTI-ALLERGY TREATMENT

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 14TH FLOOR, 2200 CLARENDON BOULEVARD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: USA

; ZIP: 22201-3360

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/480,505

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/102,692

; FILING DATE:

; APPLICATION NUMBER: US 07/776,380

; FILING DATE: 26-NOV-1991

; APPLICATION NUMBER: GB 8913737.6

; FILING DATE: 15-JUN-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/GB90/00926

; FILING DATE: 15-JUN-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: MITCHARD, LEONARD C

; REGISTRATION NUMBER: 29,009

; REFERENCE/DOCKET NUMBER: 604-176

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 875-0400

; TELEFAX: (703) 525-3468
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; FRAGMENT TYPE: internal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Fc region of human immunoglobulin E
 ; PUBLICATION INFORMATION:
 ; AUTHORS: Bennich, H
 ; AUTHORS: Bahr-Lindstrom, H
 ; JOURNAL: Prog. Immunol.
 ; VOLUME: 11
 ; PAGES: 49-58
 ; DATE: 1978
 US-08-480-505-1

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKT 4
 |||
 Db 1 RKT 3

RESULT 9

US-08-428-488-17

; Sequence 17, Application US/08428488
 ; Patent No. 5624894
 ; GENERAL INFORMATION:
 ; APPLICANT: BODOR, Nicholas S.
 ; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
 ; TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
 ; NUMBER OF SEQUENCES: 107
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis
 ; STREET: P.O. Box 1404
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/428,488
 ; FILING DATE: 27-APR-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Baumeister, Mary Katherine
 ; REGISTRATION NUMBER: 26,254

```

; REFERENCE/DOCKET NUMBER: 028724-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Position 1 = p-Glu."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "Position 11 = Met-NH2."
US-08-428-488-17

```

```

Query Match          . 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 SKD 11
      |||
Db      3 SKD 5

```

RESULT 10

US-08-256-771-27

```

; Sequence 27, Application US/08256771
; Patent No. 5656591
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
; TITLE OF INVENTION: PRODUCTS THEREWITH
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,771
; FILING DATE: July 22, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

```


; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-256-771-27

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KTR 5
|||
Db 1 KTR 3

RESULT 11

US-08-445-745-122
; Sequence 122, Application US/08445745
; Patent No. 5672585
; GENERAL INFORMATION:
; APPLICANT: Pierschbacher, Michael D.
; APPLICANT: Cheng, Soan
; APPLICANT: Craig, William S.
; APPLICANT: Tschoopp, Juerg F.
; TITLE OF INVENTION: Methods and Composition for Treating
; TITLE OF INVENTION: Thrombosis
; NUMBER OF SEQUENCES: 168
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,745
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/171,068

```

; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: US 08/079,441
; FILING DATE: 18-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,73614
; FILING DATE: 14-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,119
; FILING DATE: 05-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/506,444
; FILING DATE: 06-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9829
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 2
; OTHER INFORMATION: /note= "Xaa = (orn)"
US-08-445-745-122

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 RER 7
      |||
Db      9 RER 11

```

RESULT 12

US-08-615-181-84

; Sequence 84, Application US/08615181

; Patent No. 5756666

; GENERAL INFORMATION:

; APPLICANT: MASAFUMI, TAKIGUCHI

; APPLICANT: MIWA, KIYOSHI

; TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE

; TITLE OF INVENTION: RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND

; TITLE OF INVENTION: CURING AIDS

; NUMBER OF SEQUENCES: 115

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

```

; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,181
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/01756
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 261302/1993
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-796-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-08-615-181-84

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      7 RKS 9
      |||
Db      7 RKS 9

```

RESULT 13

US-08-191-338A-15

```

; Sequence 15, Application US/08191338A
; Patent No. 5763164
; GENERAL INFORMATION:
; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: Immunogenic Cancer Proteins and Peptides
; TITLE OF INVENTION: and Method of Use
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5763164th Clark Street, Suite 800
; CITY: Chicago
; STATE: IL

```

```

; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/191,338A
; FILING DATE: 12-JAN-1994
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5763164thrup, Thomas E.
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: nwun:002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-744-0090
; TELEFAX: 312-755-4489
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Xaa
; LOCATION: 5
; IDENTIFICATION METHOD: Phosphorylated Tyrosine
US-08-191-338A-15

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 SKD 11
      |||
Db      6 SKD 8

```

RESULT 14

```

US-08-408-604A-33
; Sequence 33, Application US/08408604A
; Patent No. 5801149
; GENERAL INFORMATION:
; APPLICANT: Shoelson, Steven
; TITLE OF INVENTION: INHIBITION OF SIGNAL TRANSDUCTION MOLECULES
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

;    COMPUTER:  IBM PC compatible
;    OPERATING SYSTEM:  PC-DOS/MS-DOS
;    SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;    APPLICATION NUMBER:  US/08/408,604A
;    FILING DATE:  21-MAR-1995
;    CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  US 08/134,558
;    FILING DATE:  08-OCT-1993
;    PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  US 07/959,949
;    FILING DATE:  09-OCT-1992
;    PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  US 07/722,359
;    FILING DATE:  19-JUNE-1991
;    ATTORNEY/AGENT INFORMATION:
;    NAME:  Myers, Louis
;    REGISTRATION NUMBER:  35,965
;    REFERENCE/DOCKET NUMBER:  JDP-014CP3
;    TELECOMMUNICATION INFORMATION:
;    TELEPHONE:  (617)227-7400
;    TELEFAX:  (617)227-5941
;    INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;    LENGTH:  11
;    TYPE:  amino acid
;    STRANDEDNESS:  single
;    TOPOLOGY:  linear
US-08-408-604A-33

```

```

Query Match          27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.1e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      9 SKD 11
      |||
Db      8 SKD 10

```

RESULT 15

```

US-08-408-604A-79
; Sequence 79, Application US/08408604A
; Patent No. 5801149
;    GENERAL INFORMATION:
;    APPLICANT:  Shoelson, Steven
;    TITLE OF INVENTION:  INHIBITION OF SIGNAL TRANSDUCTION MOLECULES
;    NUMBER OF SEQUENCES:  211
;    CORRESPONDENCE ADDRESS:
;    ADDRESSEE:  LAHIVE & COCKFIELD
;    STREET:  60 State Street, Suite 510
;    CITY:  Boston
;    STATE:  Massachusetts
;    COUNTRY:  USA
;    ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;    MEDIUM TYPE:  Floppy disk

```

```

;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/408,604A
;   FILING DATE:  21-MAR-1995
;   CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/134,558
;   FILING DATE:  08-OCT-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/959,949
;   FILING DATE:  09-OCT-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/722,359
;   FILING DATE:  19-JUNE-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Myers, Louis
;   REGISTRATION NUMBER:  35,965
;   REFERENCE/DOCKET NUMBER:  JDP-014CP3
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (617)227-7400
;   TELEFAX:  (617)227-5941
;   INFORMATION FOR SEQ ID NO:  79:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
;   FRAGMENT TYPE:  internal
US-08-408-604A-79

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 SKD 11
      |||
Db      8 SKD 10

```

RESULT 16

US-08-633-760-37

```

; Sequence 37, Application US/08633760
; Patent No. 5804429
; GENERAL INFORMATION:
;   APPLICANT:  NIWA, MINEO
;   APPLICANT:  SAITO, YOSHIMASA
;   APPLICANT:  FUJIMURA, TAKAO
;   APPLICANT:  ISHII, YOSHINORI
;   APPLICANT:  NOGUCHI, YUJI
;   TITLE OF INVENTION:  A NEW CEPHALOSPORIN C ACYLASE
;   NUMBER OF SEQUENCES:  64
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;   ADDRESSEE:  P.C.
;   STREET:  1755 JEFFERSON DAVIS HIGHWAY, SUITE 400

```

```

;   CITY:  ARLINGTON
;   STATE:  VIRGINIA
;   COUNTRY:  USA
;   ZIP:  22202
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/633,760
;   FILING DATE:  01-MAY-1996
;   CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  OBLON, NORMAN F.
;   REGISTRATION NUMBER:  24,618
;   REFERENCE/DOCKET NUMBER:  18-929-0 PCT
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (703) 413-3000
;   TELEFAX:  (703) 413-2220
;   TELEX:  248855 OPAT UR
;   INFORMATION FOR SEQ ID NO:  37:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-633-760-37

```

```

Query Match          27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.1e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      3 KTR 5
      |||
Db      5 KTR 7

```

```

RESULT 17
US-08-381-984-31
; Sequence 31, Application US/08381984
; Patent No. 5804555
;   GENERAL INFORMATION:
;   APPLICANT:  Mamoru TOMITA et al.
;   TITLE OF INVENTION:  ANTIOXIDANT
;   NUMBER OF SEQUENCES:  32
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Wenderoth, Lind & Ponack
;   STREET:  805 Fifteenth Street, N.W., #700
;   CITY:  Washington
;   STATE:  D.C.
;   COUNTRY:  U.S.A.
;   ZIP:  20005
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 mb
;   COMPUTER:  IBM Compatible

```

```

;   OPERATING SYSTEM:  MS-DOS
;   SOFTWARE:  Wordperfect 5.1
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/381,984
;   FILING DATE:  April 11, 1995
;   CLASSIFICATION:  252
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Warren M. Cheek, Jr.
;   REGISTRATION NUMBER:  33,367
;   REFERENCE/DOCKET NUMBER:
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  202-371-8850
;   TELEFAX:
;   TELEX:
;   INFORMATION FOR SEQ ID NO:  31:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   IDENTIFICATION METHOD:
;   OTHER INFORMATION:  /note= "the specified peptide as well as
;   OTHER INFORMATION:  peptides including the specified peptide as a
fragment thereof"
US-08-381-984-31

```

```

Query Match          27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.1e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      3 KTR 5
      |||
Db      1 KTR 3

```

```

RESULT 18
US-08-737-085A-12
; Sequence 12, Application US/08737085A
; Patent No. 5869232
; GENERAL INFORMATION:
; APPLICANT:  SALLBERG, MATTI
; TITLE OF INVENTION:  ANTIGEN/ANTIBODY SPECIFICITY
; TITLE OF INVENTION:  EXCHANGER
; NUMBER OF SEQUENCES:  23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  DARBY & DARBY PC
; STREET:  805 Third Avenue
; CITY:  New York
; STATE:  New York
; COUNTRY:  USA

```



```

; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,085A
; FILING DATE: 27-DEC-1996
; CLASSIFICATION: 426
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 3846/0C569
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7659
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-737-085A-12

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 RKT 4
      |||
Db      2 RKT 4

```

RESULT 19

US-07-737-371E-73

; Sequence 73, Application US/07737371E

; Patent No. 5876948

; GENERAL INFORMATION:

; APPLICANT: Yankner, Bruce A.

; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY

; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)

; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

```

;   COMPUTER:  IBM Compatible
;   OPERATING SYSTEM:  Windows95
;   SOFTWARE:  FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/07/737,371E
;   FILING DATE:  29-JUL-1991
;   CLASSIFICATION:  536
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  07/559,172
;   FILING DATE:  27-JUL-1990
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Freeman, John W.
;   REGISTRATION NUMBER:  29,066
;   REFERENCE/DOCKET NUMBER:  00108/028002
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  617-542-5070
;   TELEFAX:  617-542-8906
;   TELEX:  200154
;   INFORMATION FOR SEQ ID NO:  73:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-07-737-371E-73

```

```

Query Match          27.3%;  Score 3;  DB 2;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.1e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      9 SKD 11
      |||
Db      3 SKD 5

```

```

RESULT 20
US-08-466-975A-3
; Sequence 3, Application US/08466975A
; Patent No. 5910404
; GENERAL INFORMATION:
;   APPLICANT:  DELEYS, ROBERT J
;   APPLICANT:  POLLET, DIRK
;   APPLICANT:  MAERTENS, GEERT
;   APPLICANT:  VAN HEUVERSWUN, HUGO
;   TITLE OF INVENTION:  SYNTHETIC ANTIGENS FOR THE DETECTION OF
;   TITLE OF INVENTION:  ANTIBODIES TO HEPATITIS C VIRUS
;   NUMBER OF SEQUENCES:  23
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  NIXON & VANDERHYE P.C.
;   STREET:  1100 NORTH GLEBE ROAD
;   CITY:  ARLINGTON
;   STATE:  VA
;   COUNTRY:  USA
;   ZIP:  22201
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible

```

```

;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/466,975A
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/391,671
;   FILING DATE:
;   APPLICATION NUMBER:  US 07/920,286
;   FILING DATE:  14-OCT-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  WO PCT/EP91/02409
;   FILING DATE:  13-DEC-1991
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  EP 90124241.2
;   FILING DATE:  14-DEC-1990
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  SADOFF, B.J.
;   REGISTRATION NUMBER:  36,663
;   REFERENCE/DOCKET NUMBER:  1487-5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  7038164000
;   TELEFAX:  7038164100
;   INFORMATION FOR SEQ ID NO:  3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-466-975A-3

```

```

Query Match          27.3%;  Score 3;  DB 2;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.1e+03;
Matches      3;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy      2 RKT 4
      |||
Db      2 RKT 4

```

RESULT 21

US-08-391-671A-3

```

; Sequence 3, Application US/08391671A
; Patent No. 5922532
; GENERAL INFORMATION:
; APPLICANT:  DELEYS, ROBERT J
; APPLICANT:  POLLET, DIRK
; APPLICANT:  MAERTENS, GEERT
; APPLICANT:  VAN HEUVERSWUN, HUGO
; TITLE OF INVENTION:  SYNTHETIC ANTIGENS FOR THE DETECTION OF
; TITLE OF INVENTION:  ANTIBODIES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES:  23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  NIXON & VANDERHYE P.C.
; STREET:  1100 NORTH GLEBE ROAD

```

```

; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,671A
; FILING DATE: 21-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/920,286
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP91/02409
; FILING DATE: 13-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90124241.2
; FILING DATE: 14-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-391-671A-3

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 RKT 4
      |||
Db      2 RKT 4

```

RESULT 22

US-08-747-137-63

```

; Sequence 63, Application US/08747137
; Patent No. 5945033
; GENERAL INFORMATION:
; APPLICANT: YEN, Richard C.K.
; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:

```

```

;   ADDRESSEE:  Townsend and Townsend and Crew LLP
;   STREET:  Two Embarcadero Center, 8th Floor
;   CITY:  San Francisco
;   STATE:  CA
;   COUNTRY:  USA
;   ZIP:  94111
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/747,137
;   FILING DATE:  12-NOV-1996
;   CLASSIFICATION:  424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/212,546
;   FILING DATE:  14-MAR-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/069,831
;   FILING DATE:  01-JUN-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/959,560
;   FILING DATE:  13-OCT-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/641,720
;   FILING DATE:  15-JAN-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Apple, Randolph T.
;   REGISTRATION NUMBER:  36,429
;   REFERENCE/DOCKET NUMBER:  016197-000840US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  415-576-0200
;   INFORMATION FOR SEQ ID NO:  63:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  not relevant
;   TOPOLOGY:  not relevant
US-08-747-137-63

```

```

Query Match          27.3%;  Score 3;  DB 2;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.1e+03;
Matches      3;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

```

```

Qy          7 RKS 9
            |||
Db          5 RKS 7

```

RESULT 23

US-08-482-228-200

; Sequence 200, Application US/08482228

; Patent No. 5968753

; GENERAL INFORMATION:

; APPLICANT: Tseng-Law, Janet

; APPLICANT: Kobori, Joan A.

```

; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Guillermo, Roy
; APPLICANT: Helgerson, Sam L.
; APPLICANT: Deans, Robert J.
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
; NUMBER OF SEQUENCES: 215
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janice Guthrie, Ph.D.
; STREET: P.O. Box 15210
; CITY: Irvine
; STATE: California
; COUNTRY: USA
; ZIP: 92713-5210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,228
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Guthrie, Janice
; REGISTRATION NUMBER: 35,170
; REFERENCE/DOCKET NUMBER: IT-4630CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 440-5353
; TELEFAX: (714) 553-1952
; INFORMATION FOR SEQ ID NO: 200:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-482-228-200

```

```

Query Match      27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 SKD 11
      |||
Db      9 SKD 11

```

RESULT 24

US-08-751-767A-29

```

; Sequence 29, Application US/08751767A
; Patent No. 5994104
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, ROBERT J.
; APPLICANT: GRANT, HUGH
; APPLICANT: MACDONALD, IAN D.
; TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
; NUMBER OF SEQUENCES: 80

```

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE P.C.
 ; STREET: 1100 NORTH GLEBE ROAD
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22201
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/751,767A
 ; FILING DATE: 08-NOV-1996
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SADOFF, B.J.
 ; REGISTRATION NUMBER: 36,663
 ; REFERENCE/DOCKET NUMBER: 117-221
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 7038164091
 ; TELEFAX: 7038164100
 ; INFORMATION FOR SEQ ID NO: 29:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-751-767A-29

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKS 9
 |||
 Db 2 RKS 4

RESULT 25
 US-09-115-209-74
 ; Sequence 74, Application US/09115209
 ; Patent No. 5998375
 ; GENERAL INFORMATION:
 ; APPLICANT: Thogersen, Henning
 ; APPLICANT: Madsen, Kjeld
 ; APPLICANT: Olsen, Uffe B.
 ; APPLICANT: Johansen, Nils L.
 ; APPLICANT: Scheideler, Mark
 ; TITLE OF INVENTION: No. 5998375iceptin Analogues
 ; FILE REFERENCE: 5285.200-US
 ; CURRENT APPLICATION NUMBER: US/09/115,209
 ; CURRENT FILING DATE: 1998-07-14
 ; EARLIER APPLICATION NUMBER: 0867/97
 ; EARLIER FILING DATE: 1997-07-15
 ; EARLIER APPLICATION NUMBER: 60/052,862

; EARLIER FILING DATE: 1997-07-17
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: Xaa at position 10 is Orn
US-09-115-209-74

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARK 3
|||
Db 7 ARK 9

RESULT 26

US-08-467-902A-3

; Sequence 3, Application US/08467902A
; Patent No. 6007982
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT J
; APPLICANT: POLLET, DIRK
; APPLICANT: MAERTENS, GEERT
; APPLICANT: VAN HEUVERSWUN, HUGO
; TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF
; TITLE OF INVENTION: ANTIBODIES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,902A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,671
; FILING DATE:
; APPLICATION NUMBER: US 07/920,286
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP91/02409
; FILING DATE: 13-DEC-1991
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 90124241.2
 ; FILING DATE: 14-DEC-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SADOFF, B.J.
 ; REGISTRATION NUMBER: 36,663
 ; REFERENCE/DOCKET NUMBER: 1487-5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 7038164000
 ; TELEFAX: 7038164100
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-467-902A-3

Query Match 27.3%; Score 3; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKT 4
 |||
 Db 2 RKT 4

RESULT 27

US-08-482-528-200
 ; Sequence 200, Application US/08482528
 ; Patent No. 6017719
 ; GENERAL INFORMATION:
 ; APPLICANT: Tseng-Law, Janet
 ; APPLICANT: Kobori, Joan A.
 ; APPLICANT: Al-Abdaly, Fahad A.
 ; APPLICANT: Guillermo, Roy
 ; APPLICANT: Helgerson, Sam L.
 ; APPLICANT: Deans, Robert J.
 ; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
 ; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
 ; NUMBER OF SEQUENCES: 215
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Janice Guthrie, Ph.D.
 ; STREET: P.O. Box 15210
 ; CITY: Irvine
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92713-5210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/482,528
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435

```

; ATTORNEY/AGENT INFORMATION:
;   NAME: Guthrie, Janice
;   REGISTRATION NUMBER: 35,170
;   REFERENCE/DOCKET NUMBER: IT-4630CIP4
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (714) 440-5353
;   TELEFAX: (714) 553-1952
; INFORMATION FOR SEQ ID NO: 200:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 11 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-482-528-200

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 SKD 11
        |||
Db      9 SKD 11

```

RESULT 28

US-09-246-258-12

```

; Sequence 12, Application US/09246258
; Patent No. 6040137
; GENERAL INFORMATION:
;   APPLICANT: SALLBERG, MATTI
;   TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
;   TITLE OF INVENTION: EXCHANGER
;   NUMBER OF SEQUENCES: 23
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: DARBY & DARBY PC
;     STREET: 805 Third Avenue
;     CITY: New York
;     STATE: New York
;     COUNTRY: USA
;     ZIP: 10022
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/246,258
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/737,085
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Green, Reza
;     REGISTRATION NUMBER: 38,475
;     REFERENCE/DOCKET NUMBER: 3846/0C569
;   TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 212-527-7659
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-246-258-12

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKT 4
|||
Db 2 RKT 4

RESULT 29

US-08-444-818-105

; Sequence 105, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 105:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-444-818-105

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RER 7
|||
Db 4 RER 6

RESULT 30

US-08-392-542-4

; Sequence 4, Application US/08392542
; Patent No. 6169073
; GENERAL INFORMATION:
; APPLICANT: Halazonetis, Thanos
; APPLICANT: Hartwig, Wolfgang
; TITLE OF INVENTION: Peptides nad Peptidomimetics with
; TITLE OF INVENTION: Structural Similarity to Human p53 That Activate p53
; TITLE OF INVENTION: Function
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,542
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske, Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 0486.48439
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9100
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-392-542-4

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KSK 10
|||
Db 8 KSK 10

RESULT 31

US-08-392-542-13

; Sequence 13, Application US/08392542

; Patent No. 6169073

; GENERAL INFORMATION:

; APPLICANT: Halazonetis, Thanos

; APPLICANT: Hartwig, Wolfgang

; TITLE OF INVENTION: Peptides nad Peptidomimetics with

; TITLE OF INVENTION: Structural Similarity to Human p53 That Activate p53

; TITLE OF INVENTION: Function

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Banner, Birch, McKie & Beckett

; STREET: 1001 G Street, N.W.

; CITY: Washington, D.C.

; STATE: District of Columbia

; COUNTRY: U.S.

; ZIP: 20001

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/392,542

; FILING DATE:

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Posorske, Laurence H.

; REGISTRATION NUMBER: 34,698

; REFERENCE/DOCKET NUMBER: 0486.48439

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202 508-9100

; TELEFAX: 202 508-9299

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-392-542-13

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KSK 10

Db |||
 2 KSK 4

RESULT 32

US-08-602-999A-283

; Sequence 283, Application US/08602999A

; Patent No. 6184205

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,999A

; FILING DATE: 16-FEB-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 283:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-602-999A-283

Query Match 27.3%; Score 3; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KTR 5

|||

RESULT 33

US-08-652-877-73

; Sequence 73, Application US/08652877

; Patent No. 6187548

; GENERAL INFORMATION:

; APPLICANT: Akerstrom, Goran

; APPLICANT: Juhlin, Claes

; APPLICANT: Rask, Lars

; APPLICANT: Crumley, Gregg R.

; APPLICANT: Morse, Clarence C.

; APPLICANT: Murray, Edward M.

; APPLICANT: Hjalm, Goran

; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments

; TITLE OF INVENTION: Thereof and DNA Encoding Same

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rorer Inc.

; STREET: 500 Arcola Rd., 3C43

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426-0107

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: System 7.5.1

; SOFTWARE: Word 6.0 (Patentin)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/652,877

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/15203

; FILING DATE: 22-NOV-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/344,836

; FILING DATE: 23-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/487,314

; FILING DATE: 07-JUNE-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Savitzky, Martin

; REGISTRATION NUMBER: 29,699

; REFERENCE/DOCKET NUMBER: A1355E-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-454-3816

; TELEFAX: 610-454-3808

; INFORMATION FOR SEQ ID NO: 73:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-652-877-73

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TRE 6
|||
Db 3 TRE 5

RESULT 34

US-09-208-966-3
; Sequence 3, Application US/09208966
; Patent No. 6221355
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48881/1742
; CURRENT APPLICATION NUMBER: US/09/208,966
; CURRENT FILING DATE: 1998-12-10
; EARLIER APPLICATION NUMBER: 60/082,402
; EARLIER FILING DATE: 1998-04-20
; EARLIER APPLICATION NUMBER: 60/069,012
; EARLIER FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human
US-09-208-966-3

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 2 ARK 4

RESULT 35

US-08-647-405B-3
; Sequence 3, Application US/08647405B
; Patent No. 6228654
; GENERAL INFORMATION:
; APPLICANT: Chait, Brian T.
; APPLICANT: Zhao, Yingming
; APPLICANT: Kent, Stephen B.H.
; TITLE OF INVENTION: METHODS FOR STRUCTURE ANALYSIS OF OLIGOSACCHARIDES
; FILE REFERENCE: Oligosaccharides
; CURRENT APPLICATION NUMBER: US/08/647,405B
; CURRENT FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Related to
; OTHER INFORMATION: human translationally controlled tumor protein
US-08-647-405B-3

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 3 ARK 5

RESULT 36

US-08-647-405B-4
; Sequence 4, Application US/08647405B
; Patent No. 6228654
; GENERAL INFORMATION:
; APPLICANT: Chait, Brian T.
; APPLICANT: Zhao, Yingming
; APPLICANT: Kent, Stephen B.H.
; TITLE OF INVENTION: METHODS FOR STRUCTURE ANALYSIS OF OLIGOSACCHARIDES
; FILE REFERENCE: Oligosaccharides
; CURRENT APPLICATION NUMBER: US/08/647,405B
; CURRENT FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Related to
; OTHER INFORMATION: human translationally controlled tumor protein
US-08-647-405B-4

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 3 ARK 5

RESULT 37

US-08-647-405B-6
; Sequence 6, Application US/08647405B
; Patent No. 6228654
; GENERAL INFORMATION:
; APPLICANT: Chait, Brian T.

```
; APPLICANT: Zhao, Yingming
; APPLICANT: Kent, Stephen B.H.
; TITLE OF INVENTION: METHODS FOR STRUCTURE ANALYSIS OF OLIGOSACCHARIDES
; FILE REFERENCE: Oligosaccharides
; CURRENT APPLICATION NUMBER: US/08/647,405B
; CURRENT FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Related to
; OTHER INFORMATION: human translationally controlled tumor protein
US-08-647-405B-6
```

```
Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy          9 SKD 11
            |||
Db          3 SKD 5
```

RESULT 38

```
US-09-177-249-212
; Sequence 212, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; TITLE OF INVENTION: Development in Plants
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-212
```

```
Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 7 RKS 9
|||
Db 2 RKS 4

RESULT 39

US-09-177-249-253

; Sequence 253, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; TITLE OF INVENTION: Development in Plants
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 253
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-253

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ERK 8
|||
Db 5 ERK 7

RESULT 40

US-08-476-515A-73

; Sequence 73, Application US/08476515A
; Patent No. 6239270
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjalms, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same

```

;   NUMBER OF SEQUENCES:  84
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Martin Savitzky
;     STREET:  Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
;     STREET:  3C43,
;     CITY:  Collegeville
;     STATE:  PA
;     COUNTRY:  USA
;     ZIP:  19426-0107
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  Compaq PC
;     OPERATING SYSTEM:  Windows 95
;     SOFTWARE:  Word 7.0 (Patentin)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/476,515A
;     FILING DATE:  07-JUN-1995
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/344,836
;     FILING DATE:  23-NOV-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  WO PCT/SE94/00483
;     FILING DATE:  24-MAY-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  SE 9301764-8
;     FILING DATE:  24-MAY-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Savitzky, Martin
;     REGISTRATION NUMBER:  29,699
;     REFERENCE/DOCKET NUMBER:  A1355D
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  610-454-3816
;     TELEFAX:  610-454-3808
;   INFORMATION FOR SEQ ID NO:  73:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  11 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:  internal
US-08-476-515A-73

```

```

Query Match          27.3%;  Score 3;  DB 3;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.1e+03;
Matches      3;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy          4 TRE 6
            |||
Db          3 TRE 5

```

```

RESULT 41
US-08-894-327-4
; Sequence 4, Application US/08894327

```

```

; Patent No. 6245886
; GENERAL INFORMATION:
; APPLICANT: Halazonetis, Thanos
; APPLICANT: Hartwig, Wolfgang
; TITLE OF INVENTION: Peptides and peptidomimetics with
; TITLE OF INVENTION: structural similarity to human p53 that activate p53
; TITLE OF INVENTION: function
; FILE REFERENCE: 2973.19998
; CURRENT APPLICATION NUMBER: US/08/894,327
; CURRENT FILING DATE: 1997-12-04
; EARLIER APPLICATION NUMBER: pctus96/01535
; EARLIER FILING DATE: 1996-02-16
; EARLIER APPLICATION NUMBER: 08/392,542
; EARLIER FILING DATE: 1995-02-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-894-327-4

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 KSK 10
      |||
Db      8 KSK 10

```

```

RESULT 42
US-08-894-327-13
; Sequence 13, Application US/08894327
; Patent No. 6245886
; GENERAL INFORMATION:
; APPLICANT: Halazonetis, Thanos
; APPLICANT: Hartwig, Wolfgang
; TITLE OF INVENTION: Peptides and peptidomimetics with
; TITLE OF INVENTION: structural similarity to human p53 that activate p53
; TITLE OF INVENTION: function
; FILE REFERENCE: 2973.19998
; CURRENT APPLICATION NUMBER: US/08/894,327
; CURRENT FILING DATE: 1997-12-04
; EARLIER APPLICATION NUMBER: pctus96/01535
; EARLIER FILING DATE: 1996-02-16
; EARLIER APPLICATION NUMBER: 08/392,542
; EARLIER FILING DATE: 1995-02-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic, modified from Homo sapiens p53
US-08-894-327-13

```

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KSK 10
|||
Db 2 KSK 4

RESULT 43

US-09-532-106-12

; Sequence 12, Application US/09532106
; Patent No. 6245895
; GENERAL INFORMATION:
; APPLICANT: SALLBERG, MATTI
; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
; EXCHANGER
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DARBY & DARBY PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/532,106
; FILING DATE: 21-Mar-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,085A
; FILING DATE: 27-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 3846/0C569
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7659
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-532-106-12

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKT 4
|||
Db 2 RKT 4

RESULT 44

US-09-275-265-3

; Sequence 3, Application US/09275265

; Patent No. 6287761

; GENERAL INFORMATION:

; APPLICANT: DELEYS, ROBERT J

; APPLICANT: POLLET, DIRK

; APPLICANT: MAERTENS, GEERT

; APPLICANT: VAN HEUVERSWUN, HUGO

; TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF

; TITLE OF INVENTION: ANTIBODIES TO HEPATITIS C VIRUS

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22201

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/275,265

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/391,671

; FILING DATE: 21-FEB-1995

; APPLICATION NUMBER: US 07/920,286

; FILING DATE: 14-OCT-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/EP91/02409

; FILING DATE: 13-DEC-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 90124241.2

; FILING DATE: 14-DEC-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: SADOFF, B.J.

; REGISTRATION NUMBER: 36,663

; REFERENCE/DOCKET NUMBER: 1487-5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 7038164000

; TELEFAX: 7038164100

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-275-265-3

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKT 4
|||
Db 2 RKT 4

RESULT 45

US-08-456-466-100

; Sequence 100, Application US/08456466
; Patent No. 6395873

; GENERAL INFORMATION:

; APPLICANT: Pierschbacher, Michael D.
; Lukeman, David S.
; Cheng, Soan
; Craig, William S.
; Tschopp, Juerg F.

; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATING
; THROMBOSIS

; NUMBER OF SEQUENCES: 120

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/456,466
; FILING DATE: 01-Jun-1995
; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1537

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 100:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: circular

; FEATURE:

; NAME/KEY: Modified-site
; LOCATION: 2
; OTHER INFORMATION: /note= "Xaa=(orn)"
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-08-456-466-100

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RER 7
|||
Db 9 RER 11

RESULT 46

US-09-311-626B-30
; Sequence 30, Application US/09311626B
; Patent No. 6399347
; GENERAL INFORMATION:
; APPLICANT: Jorgensen, Per Lina
; APPLICANT: Schnorr, Kirk
; APPLICANT: Andersen, Lene No. 6399347boe
; APPLICANT: Schulein, Martin
; APPLICANT: Outtrup, Helle
; TITLE OF INVENTION: No. 6399347el Rhamnogalacturonan Hydrolases
; FILE REFERENCE: 5572.204-US
; CURRENT APPLICATION NUMBER: US/09/311,626B
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 0608/98
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: 60/084,358
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Microbial
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6
; OTHER INFORMATION: Xaa= Ser or Thr
US-09-311-626B-30

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SKD 11
|||
Db 8 SKD 10

RESULT 47

US-09-685-027-4
; Sequence 4, Application US/09685027

```

; Patent No. 6420118
; GENERAL INFORMATION:
;   APPLICANT: Halazonetis, Thanos
;               Hartwig, Wolfgang
;   TITLE OF INVENTION: Peptides nad Peptidomimetics with
;                       Structural Similarity to Human p53 That Activate
p53
;                               Function
;   NUMBER OF SEQUENCES: 35
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Banner, Birch, McKie & Beckett
;       STREET: 1001 G Street, N.W.
;       CITY: Washington, D.C.
;       STATE: District of Columbia
;       COUNTRY: U.S.
;       ZIP: 20001
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/685,027
;       FILING DATE: 10-Oct-2000
;       CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/392,542
;       FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Posorske, Laurence H.
;       REGISTRATION NUMBER: 34,698
;       REFERENCE/DOCKET NUMBER: 0486.48439
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 202 508-9100
;       TELEFAX: 202 508-9299
;   INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 11 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-685-027-4

```

```

Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 KSK 10
      |||
Db      8 KSK 10

```

```

RESULT 48
US-09-685-027-13
; Sequence 13, Application US/09685027
; Patent No. 6420118

```

```

; GENERAL INFORMATION:
;   APPLICANT: Halazonetis, Thanos
;               Hartwig, Wolfgang
;   TITLE OF INVENTION: Peptides nad Peptidomimetics with
;                       Structural Similarity to Human p53 That Activate
p53
;                               Function
;   NUMBER OF SEQUENCES: 35
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Banner, Birch, McKie & Beckett
;       STREET: 1001 G Street, N.W.
;       CITY: Washington, D.C.
;       STATE: District of Columbia
;       COUNTRY: U.S.
;       ZIP: 20001
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/685,027
;       FILING DATE: 10-Oct-2000
;       CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/392,542
;       FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Posorske, Laurence H.
;       REGISTRATION NUMBER: 34,698
;       REFERENCE/DOCKET NUMBER: 0486.48439
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 202 508-9100
;       TELEFAX: 202 508-9299
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 11 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-685-027-13

```

```

Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 KSK 10
        |||
Db      2 KSK 4

```

```

RESULT 49
US-09-500-124-283
; Sequence 283, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:

```

```

;   APPLICANT:  SPARKS, Andrew B.
;   APPLICANT:  KAY, Brian K.
;   APPLICANT:  THORN, Judith M.
;   APPLICANT:  QUILLIAM, Lawrence A.
;   APPLICANT:  DER, Channing J.
;   APPLICANT:  FOWLKES, Dana M.
;   APPLICANT:  RIDER, James E.
;   TITLE OF INVENTION:  SH3 BINDING PEPTIDES AND METHODS OF
;   TITLE OF INVENTION:  ISOLATING AND USING SAME
;   NUMBER OF SEQUENCES:  467
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Pennie & Edmonds
;       STREET:  1155 Avenue of the Americas
;       CITY:  New York
;       STATE:  New York
;       COUNTRY:  U.S.A.
;       ZIP:  10036-2711
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/500,124
;       FILING DATE:
;       CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/602,999
;       FILING DATE:  16-FEB-1996
;   ATTORNEY/AGENT INFORMATION:
;       NAME:  Misrock, S. Leslie
;       REGISTRATION NUMBER:  18,872
;       REFERENCE/DOCKET NUMBER:  1101-202
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 790-9090
;       TELEFAX:  (212) 869-9741/8864
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  283:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH:  11 amino acids
;           TYPE:  amino acid
;           TOPOLOGY:  unknown
;       MOLECULE TYPE:  peptide
US-09-500-124-283

```

```

Query Match          27.3%;  Score 3;  DB 4;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.1e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          3 KTR 5
            |||
Db          9 KTR 11

```

```

RESULT 50
US-08-255-208A-77
; Sequence 77, Application US/08255208A

```

; Patent No. 6440656
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway Jr., Stephen R.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/255,208A
; FILING DATE: 07-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= A
; OTHER INFORMATION: /note= "Preceeding this amino acid, there may be an
amino group
; OTHER INFORMATION: an acetyl group, a 9-fluorenylmethoxy-carbonyl group,
a hydroph
; OTHER INFORMATION: group or a macromolecular carrier group."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /label= B
; OTHER INFORMATION: /note= "Following this amino acid, there may be a
carboxyl grou

; OTHER INFORMATION: an amido group, a hydrophobic group, or a
macromolecular carrier
; OTHER INFORMATION: group."
US-08-255-208A-77

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKS 9
|||
Db 5 RKS 7

RESULT 51

US-09-839-666-12

; Sequence 12, Application US/09839666
; Patent No. 6469143

; GENERAL INFORMATION:

; APPLICANT: SALLBERG, MATTI
; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
; EXCHANGER

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DARBY & DARBY PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/839,666
; FILING DATE: 19-Apr-2001
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/737,085
; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 3846/0C569

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-527-7659
; TELEFAX: 212-753-6237
; TELEX: 236687

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-839-666-12

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKT 4
|||
Db 2 RKT 4

RESULT 52

US-09-082-358B-64
; Sequence 64, Application US/09082358B
; Patent No. 6469153
; GENERAL INFORMATION:
; APPLICANT: Goff, Stephen P.
; APPLICANT: Li, Xingquiang
; TITLE OF INVENTION: EIP-1, EIP-3 GENES, ENVELOPE-INTERACTING PROTEINS,
; TITLE OF INVENTION: EIP-1, and EIP-3
; FILE REFERENCE: 0575/54804
; CURRENT APPLICATION NUMBER: US/09/082,358B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 11
; TYPE: PRT
; ORGANISM: murine
US-09-082-358B-64

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKT 4
|||
Db 1 RKT 3

RESULT 53

US-09-410-551B-57
; Sequence 57, Application US/09410551B
; Patent No. 6503737
; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTI, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
; TITLE OF INVENTION: CONSTRUCTS THEREFOR
; FILE REFERENCE: 30062-20026.00
; CURRENT APPLICATION NUMBER: US/09/410,551B
; CURRENT FILING DATE: 1999-10-01

```

; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
; OTHER INFORMATION: synthase fragment
US-09-410-551B-57

```

```

Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 RER 7
      |||
Db      5 RER 7

```

RESULT 54

```

US-09-101-272G-39
; Sequence 39, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
; APPLICANT: Nissin Food Products Co., Ltd.
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
; FILE REFERENCE: Q50979
; CURRENT APPLICATION NUMBER: US/09/101,272G
; CURRENT FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: JP 1059/1996
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: intervening sequence between formula 1 and formula 2
US-09-101-272G-39

```

```

Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 KSK 10
      |||
Db      4 KSK 6

```


RESULT 55

US-08-445-638-122

; Sequence 122, Application US/08445638

; Patent No. 6521594

; GENERAL INFORMATION:

; APPLICANT: Pierschbacher, Michael D.

; APPLICANT: Cheng, Soan

; APPLICANT: Craig, William S.

; APPLICANT: Tschopp, Juerg F.

; TITLE OF INVENTION: Methods and Composition for Treating

; TITLE OF INVENTION: Thrombosis

; NUMBER OF SEQUENCES: 168

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell and Flores

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/445,638

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/171,068

; FILING DATE: 20-DEC-1993

; APPLICATION NUMBER: US 08/079,441

; FILING DATE: 18-JUN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/050,73614

; FILING DATE: 14-APR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/681,119

; FILING DATE: 05-APR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/506,444

; FILING DATE: 06-APR-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-LA 9829

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 122:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: circular

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 2

; OTHER INFORMATION: /note= "Xaa = (orn)"
US-08-445-638-122

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RER 7
|||
Db 9 RER 11

RESULT 56

US-09-941-611-3

; Sequence 3, Application US/09941611
; Patent No. 6576417

; GENERAL INFORMATION:

; APPLICANT: DELEYS, ROBERT J
; POLLET, DIRK
; MAERTENS, GEERT
; VAN HEUVERSWUN, HUGO

; TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF
; ANTIBODIES TO HEPATITIS C VIRUS

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/941,611
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/391,671
; FILING DATE: 1995-02-21
; APPLICATION NUMBER: WO PCT/EP91/02409
; FILING DATE: 13-DEC-1991
; APPLICATION NUMBER: EP 90124241.2
; FILING DATE: 14-DEC-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 7038164000
; TELEFAX: 7038164100

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-941-611-3

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKT 4
|||
Db 2 RKT 4

RESULT 57

US-09-265-222-16

; Sequence 16, Application US/09265222
; Patent No. 6579682
; GENERAL INFORMATION:
; APPLICANT: Innerarity, Thomas
; APPLICANT: Boren, Jan
; TITLE OF INVENTION: METHODS AND TOOLS FOR IDENTIFYING
; TITLE OF INVENTION: COMPOUNDS WHICH MODULATE ATHEROSCLEROSIS BY IMPACTING
; TITLE OF INVENTION: LDL-PROTEOGLYCAN BINDING
; FILE REFERENCE: 220002059700
; CURRENT APPLICATION NUMBER: US/09/265,222
; CURRENT FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: US 60/077,618
; PRIOR FILING DATE: 1998-03-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: 6
; OTHER INFORMATION: Insertion of a single amino acid
US-09-265-222-16

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TRE 6
|||
Db 4 TRE 6

RESULT 58

US-09-535-852-1119

; Sequence 1119, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:

```
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1119
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmoglein-2 cell adhesion recognition sequence
US-09-535-852-1119
```

```
Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy      1 ARK 3
        |||
Db      9 ARK 11
```

RESULT 59

```
US-09-535-852-1159
; Sequence 1159, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1159
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmoglein-2 cell adhesion recognition sequence
US-09-535-852-1159
```

```
Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy      1 ARK 3
```

Db |||
 9 ARK 11

RESULT 60

US-09-775-052A-3

; Sequence 3, Application US/09775052A
; Patent No. 6645501
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48881/1742
; CURRENT APPLICATION NUMBER: US/09/775,052A
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/208,966
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,012
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human
US-09-775-052A-3

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
 |||
Db 2 ARK 4

RESULT 61

US-09-790-497A-39

; Sequence 39, Application US/09790497A
; Patent No. 6649735
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY
IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-16
; CURRENT APPLICATION NUMBER: US/09/790,497A
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/576,824
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22

; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-790-497A-39

Query Match: 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKT 4
|||
Db 2 RKT 4

RESULT 62

US-09-576-824A-477

; Sequence 477, Application US/09576824A
; Patent No. 6667387
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY
IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-11
; CURRENT APPLICATION NUMBER: US/09/576,824A
; CURRENT FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 477
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, amino group, or chemically modified
; OTHER INFORMATION: amino terminus

; NAME/KEY: VARIANT
; LOCATION: (11)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, OH-group, NH2-group, or a linkage
; OTHER INFORMATION: involv-ing these two groups
US-09-576-824A-477

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKT 4
|||
Db 7 RKT 9

RESULT 63

US-09-576-824A-478

; Sequence 478, Application US/09576824A
; Patent No. 6667387
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY
IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-11
; CURRENT APPLICATION NUMBER: US/09/576,824A
; CURRENT FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 478
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, amino group, or chemically modified
; OTHER INFORMATION: amino terminus
; NAME/KEY: VARIANT
; LOCATION: (11)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, OH-group, NH2-group, or a linkage
; OTHER INFORMATION: involv-ing these two groups

US-09-576-824A-478

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKT 4
|||
Db 6 RKT 8

RESULT 64

US-09-576-824A-479

; Sequence 479, Application US/09576824A
; Patent No. 6667387
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY
IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-11
; CURRENT APPLICATION NUMBER: US/09/576,824A
; CURRENT FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 479
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, amino group, or chemically modified
; OTHER INFORMATION: amino terminus
; NAME/KEY: VARIANT
; LOCATION: (11)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, OH-group, NH2-group, or a linkage
; OTHER INFORMATION: involv-ing these two groups
US-09-576-824A-479

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKT 4
 | | |
Db 5 RKT 7

RESULT 65

US-09-576-824A-480

; Sequence 480, Application US/09576824A

; Patent No. 6667387

; GENERAL INFORMATION:

; APPLICANT: De Leys, Robert

; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING

; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN

; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF

; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY
IMPORTANT

; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS

; TITLE OF INVENTION: CONTAINING THEM

; FILE REFERENCE: 2752-11

; CURRENT APPLICATION NUMBER: US/09/576,824A

; CURRENT FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 08/723,425

; PRIOR FILING DATE: 1996-09-30

; PRIOR APPLICATION NUMBER: 09/146,028

; PRIOR FILING DATE: 1993-11-22

; PRIOR APPLICATION NUMBER: PCT/EP93/00517

; PRIOR FILING DATE: 1993-03-08

; PRIOR APPLICATION NUMBER: EP 92400598.6

; PRIOR FILING DATE: 1992-03-06

; NUMBER OF SEQ ID NOS: 600

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 480

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Hepatitis C virus

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: (1)

; OTHER INFORMATION: Xaa = modified site : when present, represents an

; OTHER INFORMATION: amino acid, amino group, or chemically modified

; OTHER INFORMATION: amino terminus

; NAME/KEY: VARIANT

; LOCATION: (11)

; OTHER INFORMATION: Xaa = modified site : when present, represents an

; OTHER INFORMATION: amino acid, OH-group, NH2-group, or a linkage

; OTHER INFORMATION: involv-ing these two groups

US-09-576-824A-480

Query Match 27.3%; Score 3; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKT 4
 | | |
Db 4 RKT 6

RESULT 66

US-09-576-824A-481

; Sequence 481, Application US/09576824A

; Patent No. 6667387

; GENERAL INFORMATION:

; APPLICANT: De Leys, Robert

; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING

; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN

; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF

; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT

; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS

; TITLE OF INVENTION: CONTAINING THEM

; FILE REFERENCE: 2752-11

; CURRENT APPLICATION NUMBER: US/09/576,824A

; CURRENT FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 08/723,425

; PRIOR FILING DATE: 1996-09-30

; PRIOR APPLICATION NUMBER: 09/146,028

; PRIOR FILING DATE: 1993-11-22

; PRIOR APPLICATION NUMBER: PCT/EP93/00517

; PRIOR FILING DATE: 1993-03-08

; PRIOR APPLICATION NUMBER: EP 92400598.6

; PRIOR FILING DATE: 1992-03-06

; NUMBER OF SEQ ID NOS: 600

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 481

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Hepatitis C virus

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: (1)

; OTHER INFORMATION: Xaa = modified site : when present, represents an

; OTHER INFORMATION: amino acid, amino group, or chemically modified

; OTHER INFORMATION: amino terminus

; NAME/KEY: VARIANT

; LOCATION: (11)

; OTHER INFORMATION: Xaa = modified site : when present, represents an

; OTHER INFORMATION: amino acid, OH-group, NH2-group, or a linkage

; OTHER INFORMATION: involving these two groups

US-09-576-824A-481

Query Match 27.3%; Score 3; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKT 4

|||

Db 3 RKT 5

RESULT 67

US-09-576-824A-546

; Sequence 546, Application US/09576824A

; Patent No. 6667387

```

; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY
IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-11
; CURRENT APPLICATION NUMBER: US/09/576,824A
; CURRENT FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 546
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, amino group, or chemically modified
; OTHER INFORMATION: amino terminus
; NAME/KEY: VARIANT
; LOCATION: (11)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, OH-group, NH2-group, or a linkage
; OTHER INFORMATION: involv-ing these two groups
US-09-576-824A-546

```

```

Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy          7 RKS 9
            |||
Db          8 RKS 10

```

```

RESULT 68
US-09-576-824A-547
; Sequence 547, Application US/09576824A
; Patent No. 6667387
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF

```

```

; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY
IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-11
; CURRENT APPLICATION NUMBER: US/09/576,824A
; CURRENT FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 547
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, amino group, or chemically modified
; OTHER INFORMATION: amino terminus
; NAME/KEY: VARIANT
; LOCATION: (11)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, OH-group, NH2-group, or a linkage
; OTHER INFORMATION: involv-ing these two groups
US-09-576-824A-547

```

```

Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      7 RKS 9
      |||
Db      7 RKS 9

```

RESULT 69

```

US-09-576-824A-548
; Sequence 548, Application US/09576824A
; Patent No. 6667387
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY
IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-11

```

```

; CURRENT APPLICATION NUMBER: US/09/576,824A
; CURRENT FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 548
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Hepatitis C virus
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)
;   OTHER INFORMATION: Xaa = modified site : when present, represents an
;   OTHER INFORMATION: amino acid, amino group, or chemically modified
;   OTHER INFORMATION: amino terminus
;   NAME/KEY: VARIANT
;   LOCATION: (11)
;   OTHER INFORMATION: Xaa = modified site : when present, represents an
;   OTHER INFORMATION: amino acid, OH-group, NH2-group, or a linkage
;   OTHER INFORMATION: involv-ing these two groups
US-09-576-824A-548

```

```

Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      7 RKS 9
      |||
Db      6 RKS 8

```

RESULT 70

```

US-09-576-824A-549
; Sequence 549, Application US/09576824A
; Patent No. 6667387
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY
IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-11
; CURRENT APPLICATION NUMBER: US/09/576,824A
; CURRENT FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028

```

```

; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 549
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Hepatitis C virus
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)
;   OTHER INFORMATION: Xaa = modified site : when present, represents an
;   OTHER INFORMATION: amino acid, amino group, or chemically modified
;   OTHER INFORMATION: amino terminus
;   NAME/KEY: VARIANT
;   LOCATION: (11)
;   OTHER INFORMATION: Xaa = modified site : when present, represents an
;   OTHER INFORMATION: amino acid, OH-group, NH2-group, or a linkage
;   OTHER INFORMATION: involv-ing these two groups
US-09-576-824A-549

```

```

Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      7 RKS 9
      |||
Db      5 RKS 7

```

RESULT 71

PCT-US91-08328-13

```

; Sequence 13, Application PC/TUS9108328
; GENERAL INFORMATION:
;   APPLICANT: Ruggeri, Zaverio M.
;   APPLICANT: Houghten, Richard A.
;   TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING
;   TITLE OF INVENTION: OF ADHESION MOLECULES
;   NUMBER OF SEQUENCES: 47
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Eugene Moroz, MORGAN & FINNEGAN
;   STREET: 345 Park Avenue
;   CITY: New York
;   STATE: New York
;   COUNTRY: USA
;   ZIP: 10154
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US91/08328
;   FILING DATE: 19911107

```

```

; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/610,363
; FILING DATE: 07-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Moroz, Eugene
; REGISTRATION NUMBER: 25,237
; REFERENCE/DOCKET NUMBER: 1198 4079PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)758-4800
; TELEFAX: (212)751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Cross-links
; LOCATION: 6..>11
; OTHER INFORMATION: /note= "Sequence linked by
; OTHER INFORMATION: interchain amide bond at Lys residue with Glu
; OTHER INFORMATION: residue on Arg5-Glu-Ser-Arg-Gly-Asp-Val sequence"
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 28-JUL-1987
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US B1 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 03-JUL-1990
PCT-US91-08328-13

```

```

Query Match          27.3%; Score 3; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      7 RKS 9
      |||
Db      5 RKS 7

```

RESULT 72

PCT-US91-08328-14

; Sequence 14, Application PC/TUS9108328

; GENERAL INFORMATION:

```

; APPLICANT: Ruggeri, Zaverio M.
; APPLICANT: Houghten, Richard A.
; TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING
; TITLE OF INVENTION: OF ADHESION MOLECULES
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eugene Moroz, MORGAN & FINNEGAN
; STREET: 345 Park Avenue

```

```

;   CITY:   New York
;   STATE:  New York
;   COUNTRY: USA
;   ZIP:    10154
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US91/08328
;   FILING DATE: 19911107
;   CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/610,363
;   FILING DATE: 07-NOV-1990
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Moroz, Eugene
;   REGISTRATION NUMBER: 25,237
;   REFERENCE/DOCKET NUMBER: 1198 4079PC
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212)758-4800
;   TELEFAX: (212)751-6849
;   TELEX: 421792
;   INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: AMINO ACID
;   TOPOLOGY: unknown
;   MOLECULE TYPE: peptide
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FEATURE:
;   NAME/KEY: Cross-links
;   LOCATION: 5..>11
;   OTHER INFORMATION: /note= "Sequence linked by
;   OTHER INFORMATION: interchain amide bond at Glu residue with Lys
;   OTHER INFORMATION: residue on Arg4-Lys-Arg-Ser-Arg-Gly-Asp-Val
;   PUBLICATION INFORMATION:
;   DOCUMENT NUMBER: US 4,683,291
;   FILING DATE: 28-OCT-1985
;   PUBLICATION DATE: 28-JUL-1987
;   PUBLICATION INFORMATION:
;   DOCUMENT NUMBER: US B1 4,683,291
;   FILING DATE: 28-OCT-1985
;   PUBLICATION DATE: 03-JUL-1990
PCT-US91-08328-14

```

```

Query Match          27.3%; Score 3; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          5 RER 7
            |||
Db          4 RER 6

```


RESULT 73

PCT-US91-08328-16

; Sequence 16, Application PC/TUS9108328

; GENERAL INFORMATION:

; APPLICANT: Ruggeri, Zaverio M.

; APPLICANT: Houghten, Richard A.

; TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING

; TITLE OF INVENTION: OF ADHESION MOLECULES

; NUMBER OF SEQUENCES: 47

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Eugene Moroz, MORGAN & FINNEGAN

; STREET: 345 Park Avenue

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10154

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US91/08328

; FILING DATE: 19911107

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/610,363

; FILING DATE: 07-NOV-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Moroz, Eugene

; REGISTRATION NUMBER: 25,237

; REFERENCE/DOCKET NUMBER: 1198 4079PC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)758-4800

; TELEFAX: (212)751-6849

; TELEX: 421792

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FEATURE:

; NAME/KEY: Cross-links

; LOCATION: 4..>11

; OTHER INFORMATION: /note= "Sequence linked by

; OTHER INFORMATION: interchain amide bond at Glu residue with Lys

; OTHER INFORMATION: residue on Arg3-Lys-Arg2-Ser-Arg-Gly-Asp-Val

; PUBLICATION INFORMATION:

; DOCUMENT NUMBER: US 4,683,291

; FILING DATE: 28-OCT-1985

; PUBLICATION DATE: 28-JUL-1987

; PUBLICATION INFORMATION:

; DOCUMENT NUMBER: US B1 4,683,291

; FILING DATE: 28-OCT-1985

; PUBLICATION DATE: 03-JUL-1990
PCT-US91-08328-16

Query Match 27.3%; Score 3; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RER 7
|||
Db 3 RER 5

RESULT 74

PCT-US91-08328-18

; Sequence 18, Application PC/TUS9108328

; GENERAL INFORMATION:

; APPLICANT: Ruggeri, Zaverio M.
; APPLICANT: Houghten, Richard A.
; TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING
; TITLE OF INVENTION: OF ADHESION MOLECULES
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eugene Moroz, MORGAN & FINNEGAN
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US91/08328
; FILING DATE: 19911107
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/610,363
; FILING DATE: 07-NOV-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Moroz, Eugene
; REGISTRATION NUMBER: 25,237
; REFERENCE/DOCKET NUMBER: 1198 4079PC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)758-4800
; TELEFAX: (212)751-6849
; TELEX: 421792

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:

; NAME/KEY: Cross-links
 ; LOCATION: 3..>11
 ; OTHER INFORMATION: /note= "Sequence linked by
 ; OTHER INFORMATION: interchain amide bond at residue Glu with Lys
 ; OTHER INFORMATION: residue on Arg2-Lys-Arg3-Ser-Arg-Gly-Asp-Val
 ; PUBLICATION INFORMATION:
 ; DOCUMENT NUMBER: US 4,683,291
 ; FILING DATE: 28-OCT-1985
 ; PUBLICATION DATE: 28-JUL-1987
 ; PUBLICATION INFORMATION:
 ; DOCUMENT NUMBER: US B1 4,683,291
 ; FILING DATE: 28-OCT-1985
 ; PUBLICATION DATE: 03-JUL-1990
 PCT-US91-08328-18

Query Match 27.3%; Score 3; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RER 7
 |||
 Db 2 RER 4

RESULT 75

PCT-US91-08328-20

; Sequence 20, Application PC/TUS9108328
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruggeri, Zaverio M.
 ; APPLICANT: Houghten, Richard A.
 ; TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING
 ; TITLE OF INVENTION: OF ADHESION MOLECULES
 ; NUMBER OF SEQUENCES: 47
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Eugene Moroz, MORGAN & FINNEGAN
 ; STREET: 345 Park Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10154
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US91/08328
 ; FILING DATE: 19911107
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/610,363
 ; FILING DATE: 07-NOV-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Moroz, Eugene
 ; REGISTRATION NUMBER: 25,237
 ; REFERENCE/DOCKET NUMBER: 1198 4079PC
 ; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (212)758-4800
; TELEFAX: (212)751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Cross-links
; LOCATION: 2..>11
; OTHER INFORMATION: /note= "Sequence linked by
; OTHER INFORMATION: interchain amide bond at residue Glu with Lys
; OTHER INFORMATION: residue on Arg-Lys-Arg4-Ser-Arg-Gly-Asp-Val"
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 28-JUL-1987
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US B1 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 03-JUL-1990
PCT-US91-08328-20

```

```

Query Match          27.3%; Score 3; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      5 RER 7
      |||
Db      1 RER 3

```

```

Search completed: April 8, 2004, 15:52:11
Job time : 12.3077 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 8.61538 Seconds
(without alignments)
122.816 Million cell updates/sec

Title: US-09-787-443A-14
Perfect score: 11
Sequence: 1 ARKTRERKSKD 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 226

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	3	27.3	11	1	EOOCC	eledoisin - curled
2	3	27.3	11	1	EOOC	eledoisin - musky
3	3	27.3	11	2	B41835	translation elonga
4	3	27.3	11	2	G61497	seed protein ws-23
5	3	27.3	11	2	PU0034	dextranucrase (EC
6	2	18.2	11	2	S32575	ribosomal protein
7	2	18.2	11	2	A40693	transgelin - sheep
8	2	18.2	11	2	A26930	ermG leader peptid
9	2	18.2	11	2	YHRT	morphogenetic neur
10	2	18.2	11	2	YHHU	morphogenetic neur
11	2	18.2	11	2	YHBO	morphogenetic neur
12	2	18.2	11	2	YHXAE	morphogenetic neur
13	2	18.2	11	2	YHJFHY	morphogenetic neur

14	2	18.2	11	2	B26744	megascoliakinin -
15	2	18.2	11	2	D61033	ranatachykinin D -
16	2	18.2	11	2	S42449	antl protein - pha
17	2	18.2	11	2	JQ0395	hypothetical prote
18	2	18.2	11	2	S66606	quinoline 2-oxidor
19	2	18.2	11	2	PC2372	58K heat shock pro
20	2	18.2	11	2	PT0081	protein QA300023 -
21	2	18.2	11	2	S19775	wound-induced prot
22	2	18.2	11	2	A34135	DNA-binding protei
23	2	18.2	11	2	E57789	gallbladder stone
24	2	18.2	11	2	I52980	glucocerebrosidase
25	2	18.2	11	2	I54193	Rhesus blood group
26	2	18.2	11	2	S68637	acetylcholinestera
27	2	18.2	11	2	S78765	ribosomal protein
28	2	18.2	11	2	S54347	tubulin beta chain
29	2	18.2	11	2	A14454	6-phosphofructokin
30	2	18.2	11	2	PH1632	Ig H chain V-D-J r
31	2	18.2	11	2	PH1600	Ig H chain V-D-J r
32	2	18.2	11	2	PH1583	Ig H chain V-D-J r
33	2	18.2	11	2	PH1584	Ig H chain V-D-J r
34	2	18.2	11	2	PD0442	NIPSNAP2 protein -
35	2	18.2	11	2	PT0214	T-cell receptor be
36	2	18.2	11	2	PD0441	translation elonga
37	2	18.2	11	2	PH0939	T-cell receptor be
38	2	18.2	11	2	PH0903	T-cell receptor be
39	2	18.2	11	2	T12264	cytochrome-c oxida
40	2	18.2	11	2	T12253	cytochrome-c oxida
41	2	18.2	11	2	T12244	cytochrome-c oxida
42	2	18.2	11	2	T12248	cytochrome-c oxida
43	2	18.2	11	2	A48973	glucoamylase A1 (E
44	2	18.2	11	2	S60294	tubulin 2 beta-3 c
45	2	18.2	11	4	PC2124	aminotransferase c
46	1	9.1	11	1	XAVIBH	bradykinin-potenti
47	1	9.1	11	1	XASNBA	bradykinin-potenti
48	1	9.1	11	1	ECLQ2M	tachykinin II - mi
49	1	9.1	11	1	SPHO	substance P - hors
50	1	9.1	11	1	A60654	substance P - guin
51	1	9.1	11	1	GMROL	leucosulfakinin -
52	1	9.1	11	1	LFTWWE	probable trpEG lea
53	1	9.1	11	2	S66196	alcohol dehydrogen
54	1	9.1	11	2	G42762	proteasome endopep
55	1	9.1	11	2	S68392	H+-transporting tw
56	1	9.1	11	2	A33917	dihydroorotase (EC
57	1	9.1	11	2	B49164	chromogranin-B - r
58	1	9.1	11	2	JN0023	substance P - chic
59	1	9.1	11	2	A38841	rhodopsin homolog
60	1	9.1	11	2	PQ0682	photosystem I 17.5
61	1	9.1	11	2	S00616	parasporal crystal
62	1	9.1	11	2	C53652	rhlR protein - Pse
63	1	9.1	11	2	S09074	cytochrome P450-4b
64	1	9.1	11	2	A57458	gene Gax protein -
65	1	9.1	11	2	D60409	kassinin-like pept
66	1	9.1	11	2	F60409	substance P-like p
67	1	9.1	11	2	E60409	substance P-like p
68	1	9.1	11	2	A61365	phyllokinin - Rohd
69	1	9.1	11	2	S23308	substance P - rain
70	1	9.1	11	2	S23306	substance P - Atla

71	1	9.1	11	2	B60409	kassinin-like pept
72	1	9.1	11	2	C60409	kassinin-like pept
73	1	9.1	11	2	S07203	uperolein - frog (
74	1	9.1	11	2	S07207	Crinia-angiotensin
75	1	9.1	11	2	S07201	physalaemin - frog
76	1	9.1	11	2	A61033	ranatachykinin A -
77	1	9.1	11	2	B58501	24K kidney and bla
78	1	9.1	11	2	D58502	27K bile and gallb
79	1	9.1	11	2	A58502	38K kidney stone p
80	1	9.1	11	2	C58501	42K bile stone pro
81	1	9.1	11	2	F58501	43.5K bile stone p
82	1	9.1	11	2	PQ0231	beta-glucosidase (
83	1	9.1	11	2	S58244	pyrroloquinoline q
84	1	9.1	11	2	S04875	nifS protein - Bra
85	1	9.1	11	2	I41138	acetyl ornithine d
86	1	9.1	11	2	S42587	celF protein - Esc
87	1	9.1	11	2	S35490	type II site-speci
88	1	9.1	11	2	S21127	precorrin methyltr
89	1	9.1	11	2	S70720	trigger factor hom
90	1	9.1	11	2	S33782	acetolactate synth
91	1	9.1	11	2	B39853	LuxC protein - Pho
92	1	9.1	11	2	A58838	hemolysin - Porphy
93	1	9.1	11	2	B43669	hypothetical prote
94	1	9.1	11	2	E60691	phycobilisome 8K l
95	1	9.1	11	2	D60691	phycobilisome 9K l
96	1	9.1	11	2	S14087	parasporal crystal
97	1	9.1	11	2	A44755	20alpha-hydroxyste
98	1	9.1	11	2	E41476	probable antigen 5
99	1	9.1	11	2	A55149	tetracenomycin A2
100	1	9.1	11	2	S19301	endo-1,4-beta-xyla

ALIGNMENTS

RESULT 1

EOOCC

eledoisin - curled octopus

C;Species: Eledone cirrosa, Ozaena cirrosa (curled octopus)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Mar-1998

C;Accession: B01561; A01561

R;Anastasi, A.; Erspamer, V.

Arch. Biochem. Biophys. 101, 56-65, 1963

A;Title: The isolation and amino acid sequence of eledoisin, the active endecapeptide of the posterior salivary glands of Eledone.

A;Reference number: A01561

A;Accession: B01561

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland; secretagogue; vasodilator; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 27.3%; Score 3; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SKD 11
|||
Db 3 SKD 5

RESULT 2

EOOC

eledoisin - musky octopus

C;Species: Eledone moschata, Ozaena moschata (musky octopus)

C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 20-Mar-1998

C;Accession: A01561

R;Anastasi, A.; Erspamer, V.

Arch. Biochem. Biophys. 101, 56-65, 1963

A;Title: The isolation and amino acid sequence of eledoisin, the active endecapeptide of the posterior salivary glands of Eledone.

A;Reference number: A01561

A;Accession: A01561

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland; secretagogue; vasodilator; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SKD 11
|||
Db 3 SKD 5

RESULT 3

B41835

translation elongation factor EF-G homolog - Bacillus subtilis (fragment)

C;Species: Bacillus subtilis

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Dec-1997

C;Accession: B41835

R;Mitchell, C.; Morris, P.W.; Vary, J.C.

J. Bacteriol. 174, 2474-2477, 1992

A;Title: Identification of proteins phosphorylated by ATP during sporulation of Bacillus subtilis.

A;Reference number: A41835; MUID:92210489; PMID:1556067

A;Accession: B41835

A;Molecule type: protein

A;Residues: 1-11 <MIT>

A;Note: this protein is phosphorylated during stationary phase but not during exponential growth

C;Keywords: phosphoprotein

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KTR 5
|||
Db 5 KTR 7

RESULT 4

G61497

seed protein ws-23 - winged bean (fragment)

C;Species: Psophocarpus tetragonolobus (winged bean)

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994

C;Accession: G61497

R;Hirano, H.

J. Protein Chem. 8, 115-130, 1989

A;Title: Microsequence analysis of winged bean seed proteins electroblotted from two-dimensional gel.

A;Reference number: A61491; MUID:89351606; PMID:2765119

A;Accession: G61497

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <HIR>

C;Keywords: glycoprotein; seed

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KSK 10
|||
Db 2 KSK 4

RESULT 5

PU0034

dextranucrase (EC 2.4.1.5) - Streptococcus bovis (fragment)

C;Species: Streptococcus bovis

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 18-Sep-1996

C;Accession: PU0034

R;Uezono, Y.; Tsumori, H.; Mukasa, H.

submitted to JIPID, October 1993

A;Description: Purification and properties of glucosyltransferase synthesizing 1,6-alpha-D-glucan from Streptococcus bovis.

A;Reference number: PU0034

A;Accession: PU0034

A;Molecule type: protein

A;Residues: 1-11 <UEZ>

A;Experimental source: ATCC 9809

C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TRE 6
|||
Db 9 TRE 11

RESULT 6

S32575

ribosomal protein S2, plastid - squawroot plastid (fragment)

C;Species: plastid *Conopholis americana* (squawroot)

C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 13-Aug-1999

C;Accession: S32575

R;Taylor, G.W.; Wolfe, K.H.; Morden, C.W.; dePamphilis, C.W.; Palmer, J.D.

Curr. Genet. 20, 515-518, 1991

A;Title: Lack of a functional plastid tRNA(Cys) gene is associated with loss of photosynthesis in a lineage of parasitic plants.

A;Reference number: S32575; MUID:92145776; PMID:1723664

A;Accession: S32575

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <TAY>

A;Cross-references: EMBL:X64567; NID:g11275; PIDN:CAA45868.1; PID:g11276

C;Genetics:

A;Gene: rps2

A;Genome: plastid

C;Superfamily: *Escherichia coli* ribosomal protein S2

C;Keywords: plastid; protein biosynthesis; ribosome

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5

||

Db 2 TR 3

RESULT 7

A40693

transgelin - sheep (fragment)

C;Species: *Ovis orientalis aries*, *Ovis ammon aries* (domestic sheep)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 31-Oct-1997

C;Accession: A40693

R;Shapland, C.; Hsuan, J.J.; Totty, N.F.; Lawson, D.

J. Cell Biol. 121, 1065-1073, 1993

A;Title: Purification and properties of transgelin: a transformation and shape change sensitive actin-gelling protein.

A;Reference number: A40693; MUID:93273790; PMID:8501116

A;Accession: A40693

A;Molecule type: protein

A;Residues: 1-11 <SHA>

A;Experimental source: aorta

C;Comment: This protein gels actin and is down regulated by transformation or loss of cell adherence in culture.

C;Superfamily: smooth muscle protein SM22; calponin repeat homology; smooth muscle protein SM22 homology

C;Keywords: actin binding; cytoskeleton

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RE 6
||
Db 9 RE 10

RESULT 8

A26930

ermG leader peptide 1 - Bacillus sphaericus

C;Species: Bacillus sphaericus

C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 24-Sep-1999

C;Accession: A26930

R;Monod, M.; Mohan, S.; Dubnau, D.

J. Bacteriol. 169, 340-350, 1987

A;Title: Cloning and analysis of ermG, a new macrolide-lincosamide-streptogramin B resistance element from Bacillus sphaericus.

A;Reference number: A91840; MUID:87083389; PMID:3025178

A;Accession: A26930

A;Molecule type: DNA

A;Residues: 1-11 <MON>

A;Cross-references: GB:M15332; NID:g142881; PIDN:AAA22417.1; PID:g142882

C;Superfamily: unassigned leader peptides

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SK 10
||
Db 5 SK 6

RESULT 9

YHRT

morphogenetic neuropeptide - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: A01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birrer, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator by the authors, because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide;
pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SK 10
||
Db 6 SK 7

RESULT 10

YHHU

morphogenetic neuropeptide - human

C;Species: Homo sapiens (man)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: B01427; A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator,
from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: B01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical
structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was
called head activator because it induced head-specific growth and
differentiation in this animal. It has been found in mammalian intestine and
hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine;
neuropeptide

F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic
acid) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SK 10
||
Db 6 SK 7

RESULT 11

YHBO

morphogenetic neuropeptide - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
 C;Accession: C01427; A01427
 R;Bodenmuller, H.; Schaller, H.C.
 Nature 293, 579-580, 1981
 A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.
 A;Reference number: A93266; MUID:82035850; PMID:7290191
 A;Accession: C01427
 A;Molecule type: protein
 A;Residues: 1-11 <BOD>
 R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
 FEBS Lett. 131, 317-321, 1981
 A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
 A;Reference number: A91296; MUID:82050803; PMID:7297679
 A;Contents: annotation; synthesis
 A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity
 C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.
 C;Superfamily: unassigned animal peptides
 C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide
 F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.8e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SK 10
 ||
 Db 6 SK 7

RESULT 12

YHXAE

morphogenetic neuropeptide - sea anemone (*Anthopleura elegantissima*)

N;Alternate names: head activator

C;Species: *Anthopleura elegantissima*

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: A93900; A01427

R;Schaller, H.C.; Bodenmuller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A;Reference number: A93900

A;Accession: A93900

A;Molecule type: protein

A;Residues: 1-11 <SCH>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SK 10
||
Db 6 SK 7

RESULT 13

YHJFHY

morphogenetic neuropeptide - Hydra attenuata

N;Alternate names: head activator

C;Species: Hydra attenuata

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: B93900; A01427

R;Schaller, H.C.; Bodenmuller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A;Reference number: A93900

A;Accession: B93900

A;Molecule type: protein

A;Residues: 1-11 <SCH>

R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SK 10
||
Db 6 SK 7

RESULT 14

B26744

megascoliakinin - garden dagger wasp

N;Alternate names: 6-Thr-bradykinin-Lys-Ala

C;Species: Megascolia flavifrons (garden dagger wasp)

C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 18-Aug-2000

C;Accession: B26744; A28609

R;Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.

Toxicon 25, 527-535, 1987

A;Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp Megascolia flavifrons.

A;Reference number: A94322; MUID:87293024; PMID:3617088

A;Accession: B26744

A;Molecule type: protein

A;Residues: 1-11 <YAS>

R;Nakajima, T.; Piek, T.; Yashuara, T.; Mantel, P.

Toxicon 26, 34, 1988

A;Title: Two kinins isolated from the venom of Megascolia flavifrons.

A;Reference number: A28609

A;Accession: A28609

A;Molecule type: protein

A;Residues: 1-11 <NAK>

C;Superfamily: unassigned animal peptides

C;Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match	18.2%;	Score 2;	DB 2;	Length 11;
Best Local Similarity	100.0%;	Pred. No. 2.8e+04;		
Matches	2;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

Qy	2 RK 3
Db	9 RK 10

RESULT 15

D61033

ranatachykinin D - bullfrog

C;Species: Rana catesbeiana (bullfrog)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000

C;Accession: D61033; JE0429

R;Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.

Regul. Pept. 42(Suppl.1), S12, 1992

A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.

A;Reference number: A61033

A;Accession: D61033

A;Molecule type: protein

A;Residues: 1-11 <KAN>

R;Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.

Biochem. Biophys. Res. Commun. 177, 588-595, 1991

A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.

A;Reference number: JE0426; MUID:91254337; PMID:2043143

A;Accession: JE0429

A;Molecule type: protein

A;Residues: 1-11 <KOZ>

C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; neuropeptide
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ER 7
||
Db 5 ER 6

RESULT 16

S42449

ant1 protein - phage P7

C;Species: phage P7

C;Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 08-Oct-1999

C;Accession: S42449

R;Citron, M.; Schuster, H.

Cell 62, 591-598, 1990

A;Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.

A;Reference number: S42448; MUID:90335968; PMID:1696181

A;Accession: S42449

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-11 <CIT>

A;Cross-references: EMBL:M35139; NID:g215705; PIDN:AAA32437.1; PID:g215707

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 7 TR 8

RESULT 17

JQ0395

hypothetical protein (nodB 3' region) - Azorhizobium caulinodans

N;Alternate names: hypothetical 1.4K protein

C;Species: Azorhizobium caulinodans

A;Note: host Sesbania rostrata

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 03-Feb-1994

C;Accession: JQ0395

R;Goethals, K.; Gao, M.; Tomekpe, K.; Van Montagu, M.; Holsters, M.

Mol. Gen. Genet. 219, 289-298, 1989

A;Title: Common nodABC genes in Nod locus 1 of Azorhizobium caulinodans:
nucleotide sequence and plant-inducible expression.

A;Reference number: JQ0393; MUID:90136519; PMID:2615763

A;Accession: JQ0395

A;Molecule type: DNA

A;Residues: 1-11 <GOE>

A;Cross-references: GB:L18897

A;Experimental source: strain ORS571

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 10 AR 11

RESULT 18

S66606

quinoline 2-oxidoreductase alpha chain - Comamonas testosteroni (fragment)

C;Species: Comamonas testosteroni

C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C;Accession: S66606

R;Schach, S.; Tshisuaka, B.; Fetzner, S.; Lingens, F.

Eur. J. Biochem. 232, 536-544, 1995

A;Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from Comamonas testosteroni 63. The first two enzymes in quinoline and 3-methylquinoline degradation.

A;Reference number: S66606; MUID:96035889; PMID:7556204

A;Accession: S66606

A;Molecule type: protein

A;Residues: 1-11 <SCH>

A;Experimental source: strain 63

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KS 9
||
Db 2 KS 3

RESULT 19

PC2372

58K heat shock protein groEL [similarity] - Bacillus cereus (strain ts-4) (fragment)

C;Species: Bacillus cereus

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C;Accession: PC2372

R;Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.

Biosci. Biotechnol. Biochem. 59, 231-235, 1995

A;Title: Identification of DNA-binding proteins changed after induction of sporulation in Bacillus cereus.

A;Reference number: PC2369; MUID:95218265; PMID:7766022

A;Accession: PC2372

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <MAS>

C;Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 10 AR 11

RESULT 20

PT0081

protein QA300023 - Arabidopsis thaliana (fragment)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 24-Nov-1999

C;Accession: PT0081

R;Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.

submitted to JIPID, December 1995

A;Description: Two dimensional electrophoresis of plant proteins and
standardization of the gel patterns.

A;Reference number: PN0173

A;Accession: PT0081

A;Molecule type: protein

A;Residues: 1-11 <TSU>

A;Experimental source: Leaf

C;Keywords: acetylated amino end

F;1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SK 10
||
Db 1 SK 2

RESULT 21

S19775

wound-induced protein - tomato (fragment)

C;Species: Lycopersicon esculentum (tomato)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Sep-1997

C;Accession: S19775

R;Parsons, B.L.

submitted to the EMBL Data Library, May 1991

A;Reference number: S19773

A;Accession: S19775

A;Molecule type: mRNA

A;Residues: 1-11 <PAR>

A;Cross-references: EMBL:X59884; NID:g19323; PID:g19324

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SK 10
||
Db 4 SK 5

RESULT 22

A34135

DNA-binding protein p - Crithidia fasciculata mitochondrion (fragment)

C;Species: mitochondrion Crithidia fasciculata

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 07-Dec-1999

C;Accession: A34135

R;Tittawella, I.

FEBS Lett. 260, 57-61, 1990.

A;Title: Kinetoplast DNA-aggregating proteins from the parasitic protozoan Crithidia fasciculata.

A;Reference number: A34135

A;Accession: A34135

A;Molecule type: protein

A;Residues: 1-11 <TIT>

C;Genetics:

A;Genome: mitochondrion

A;Genetic code: SGC6

C;Keywords: mitochondrion

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3

||

Db 8 RK 9

RESULT 23

E57789

gallbladder stone matrix protein, 25K - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 23-Feb-1996

C;Accession: E57789

R;Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, February 1996

A;Description: The proteins of gallbladder stones.

A;Reference number: A57789

A;Accession: E57789

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <BIN>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5

||

Db 1 TR 2

RESULT 24

I52980

glucocerebrosidase - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C;Accession: I52980; I65971

R;Reiner, O.; Wigderson, M.; Horowitz, M.
 DNA 7, 107-116, 1988
 A;Title: Structural analysis of the human glucocerebrosidase genes.
 A;Reference number: I52980; MUID:88195776; PMID:3359914
 A;Accession: I52980
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-11 <RES>
 A;Cross-references: GB:M18916; NID:g183023; PIDN:AAA35878.1; PID:g183024
 A;Accession: I65971
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-11 <RE2>
 A;Cross-references: GB:M18917; NID:g183025; PIDN:AAA35879.1; PID:g183026

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.8e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RE 6
 ||
 Db 8 RE 9

RESULT 25

I54193
 Rhesus blood group CcEe protein - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
 C;Accession: I54193
 R;Cherif-Zahar, B.; Le Van Kim, C.; Rouillac, C.; Raynal, V.; Cartron, J.P.;
 Colin, Y.
 Genomics 19, 68-74, 1994
 A;Title: Organization of the gene (RHCE) encoding the human blood group RhCcEe
 antigens and characterization of the promoter region.
 A;Reference number: I54193; MUID:94245182; PMID:8188244
 A;Accession: I54193
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-11 <RES>
 A;Cross-references: GB:S70456; NID:g546795; PIDN:AAD14061.1; PID:g4261761
 C;Genetics:
 A;Gene: GDB:RHCE
 A;Cross-references: GDB:229957; OMIM:111700
 A;Map position: 1p36.2-1p34

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.8e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SK 10
 ||
 Db 3 SK 4

RESULT 26

S68637

acetylcholinesterase (EC 3.1.1.7) P chain - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 30-Jan-1998
C;Accession: S68637
R;Boschetti, N.; Brodbeck, U.
FEBS Lett. 380, 133-136, 1996
A;Title: The membrane anchor of mammalian brain acetylcholinesterase consists of
a single glycosylated protein of 22 kDa.
A;Reference number: S68637; MUID:96181683; PMID:8603722
A;Accession: S68637
A;Molecule type: protein
A;Residues: 1-11 <BOS>
A;Experimental source: brain
C;Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KS 9
||
Db 4 KS 5

RESULT 27

S78765
ribosomal protein MRP-S24, mitochondrial - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: S78765
R;Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A;Reference number: S78760
A;Accession: S78765
A;Molecule type: protein
A;Residues: 1-11 <GRA>
C;Keywords: mitochondrion
F;1-11/Product: ribosomal protein MRP-S24 (fragment) #status experimental <MAT>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KD 11
||
Db 7 KD 8

RESULT 28

S54347
tubulin beta chain - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 27-Oct-1995 #sequence_revision 30-Jan-1998 #text_change 07-May-1999
C;Accession: S54347
R;Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.
Biochem. J. 306, 551-555, 1995

A;Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in glial cells.

A;Reference number: S54343; MUID:95194333; PMID:7887910

A;Accession: S54347

A;Molecule type: protein

A;Residues: 1-11 <OKA>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KD 11
||
Db 1 KD 2

RESULT 29

A14454

6-phosphofructokinase (EC 2.7.1.11) - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 28-Apr-1993

C;Accession: A14454

R;Fordyce, A.M.; Midwinter, G.G.; Moore, C.H.

Biochem. Soc. Trans. 7, 721-723, 1979

A;Title: The N-terminal amino acid sequence of sheep heart phosphofructokinase.

A;Reference number: A14454; MUID:80004524; PMID:157899

A;Accession: A14454

A;Molecule type: protein

A;Residues: 1-11 <FOR>

C;Keywords: glycolysis; phosphotransferase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KT 4
||
Db 9 KT 10

RESULT 30

PH1632

Ig H chain V-D-J region (clone B-less 209) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PH1632

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1632

A;Molecule type: DNA

A;Residues: 1-11 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 2 AR 3

RESULT 31

PH1600

Ig H chain V-D-J region (wild-type clone 310) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PH1600

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1600

A;Molecule type: DNA

A;Residues: 1-11 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 2 AR 3

RESULT 32

PH1583

Ig H chain V-D-J region (wild-type clone 6) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PH1583

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1583

A;Molecule type: DNA

A;Residues: 1-11 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 2 AR 3

RESULT 33

PH1584

Ig H chain V-D-J region (wild-type clone 8) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PH1584

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1584

A;Molecule type: DNA

A;Residues: 1-11 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 2 AR 3

RESULT 34

PD0442

NIPSNAP2 protein - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 05-Feb-1999

C;Accession: PD0442

R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.
submitted to JIPID, August 1998

A;Description: Proteome analysis of mouse brain.

A;Reference number: PD0441

A;Contents: Striatum

A;Accession: PD0442

A;Molecule type: protein

A;Residues: 1-11 <KAW>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RE 6
||
Db 1 RE 2

RESULT 35

PT0214

T-cell receptor beta chain V-J region (4-1-L.6) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C;Accession: PT0214

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted in non-obese diabetic mice.

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0214

A;Molecule type: mRNA

A;Residues: 1-11 <NAK>

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 3 AR 4

RESULT 36

PD0441

translation elongation factor TU-like protein P43, mitochondrial - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 21-Aug-1998

C;Accession: PD0441

R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A. submitted to JIPID, August 1998

A;Description: Proteome analysis of mouse brain.

A;Reference number: PD0441

A;Accession: PD0441

A;Molecule type: protein

A;Residues: 1-11 <KAW>

A;Experimental source: striatum

C;Keywords: mitochondrion

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KT 4
||
Db 6 KT 7

RESULT 37

PH0939

T-cell receptor beta chain V-D-J region (clone 10) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0939
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.
 J. Exp. Med. 174, 1467-1476, 1991
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
 allergic encephalomyelitis: conserved complementarity determining region 3.
 A;Reference number: PH0891; MUID:92078857; PMID:1836012
 A;Accession: PH0939
 A;Molecule type: mRNA
 A;Residues: 1-11 <GOL>
 A;Experimental source: complete Freund's adjuvant-immunized lymph node
 C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.8e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SK 10
 ||
 Db 4 SK 5

RESULT 38

PH0903
 T-cell receptor beta chain V-D-J region (hybridoma S1C2A6) - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 C;Accession: PH0903
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.
 J. Exp. Med. 174, 1467-1476, 1991
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
 allergic encephalomyelitis: conserved complementarity determining region 3.
 A;Reference number: PH0891; MUID:92078857; PMID:1836012
 A;Accession: PH0903
 A;Molecule type: mRNA
 A;Residues: 1-11 <GOL>
 A;Experimental source: myelin basic protein-immunized T-cell
 C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.8e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ER 7
 ||
 Db 9 ER 10

RESULT 39

T12264
 cytochrome-c oxidase (EC 1.9.3.1) chain I - *Laudakia caucasia* mitochondrion
 (fragment)
 C;Species: mitochondrion *Laudakia caucasia*
 C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 03-Aug-2001
 C;Accession: T12264; T12267; T12270; T12273; T12276; T12279
 R;Macey, J.R.; Schulte II, J.A.; Ananjeva, N.B.; Larson, A.; Rastegar-Pouyani,
 N.; Shammakov, S.M.; Papenfuss, T.J.
 Mol. Phylogenet. Evol. 10, 118-131, 1998

A;Title: Phylogenetic relationships among agamid lizards of the Laudakia caucasia species group: Testing hypotheses of biogeographic fragmentation and an area cladogram for the Iranian Plateau.
 A;Reference number: Z17470; MUID:98424476; PMID:9751922
 A;Accession: T12264
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-11 <MAC1>
 A;Cross-references: EMBL:AF028681; NID:g3641460; PIDN:AAC99596.1; PID:g3641463
 A;Experimental source: specimen voucher CAS185010; California Academy of Sciences, San Francisco
 A;Accession: T12267
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-11 <MAC2>
 A;Cross-references: EMBL:AF028682; NID:g3641464; PIDN:AAC99599.1; PID:g3641467
 A;Accession: T12270
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-11 <MAC3>
 A;Cross-references: EMBL:AF028683; NID:g3641468; PIDN:AAC99602.1; PID:g3641471
 A;Accession: T12273
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-11 <MAC4>
 A;Cross-references: EMBL:AF028684; NID:g3641472; PIDN:AAC99605.1; PID:g3641475
 A;Accession: T12276
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-11 <MAC5>
 A;Cross-references: EMBL:AF028686; NID:g3641480; PIDN:AAC99611.1; PID:g3641483
 A;Accession: T12279
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-11 <MAC6>
 A;Cross-references: EMBL:AF028687; NID:g3641484; PIDN:AAC99614.1; PID:g3641487
 C;Genetics:
 A;Gene: COI
 A;Genome: mitochondrion
 C;Keywords: mitochondrion; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.8e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
 ||
 Db 5 TR 6

RESULT 40

T12253

cytochrome-c oxidase (EC 1.9.3.1) chain I - Laudakia erythrogastra mitochondrion (fragment)

C;Species: mitochondrion Laudakia erythrogastra

C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 03-Aug-2001

C;Accession: T12253; T12257

R;Macey, J.R.; Schulte II, J.A.; Ananjeva, N.B.; Larson, A.; Rastegar-Pouyani, N.; Shammakov, S.M.; Papenfuss, T.J.
Mol. Phylogenet. Evol. 10, 118-131, 1998
A;Title: Phylogenetic relationships among agamid lizards of the *Laudakia caucasia* species group: Testing hypotheses of biogeographic fragmentation and an area cladogram for the Iranian Plateau.
A;Reference number: Z17470; MUID:98424476; PMID:9751922
A;Accession: T12253
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-11 <MAC1>
A;Cross-references: EMBL:AF028679; NID:g3641452; PIDN:AAC99590.1; PID:g3641455
A;Experimental source: specimen voucher CAS182954; California Academy of Sciences, San Francisco
A;Accession: T12257
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-11 <MAC2>
A;Cross-references: EMBL:AF028680; NID:g3641456; PIDN:AAC99593.1; PID:g3641459
A;Experimental source: specimen voucher CAS184400; California Academy of Sciences, San Francisco
C;Genetics:
A;Gene: COI
A;Genome: mitochondrion
C;Keywords: mitochondrion; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 5 TR 6

RESULT 41

T12244

cytochrome-c oxidase (EC 1.9.3.1) chain I - *Laudakia lehmanni* mitochondrion (fragment)

C;Species: mitochondrion *Laudakia lehmanni*

C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 03-Aug-2001

C;Accession: T12244

R;Macey, J.R.; Schulte II, J.A.; Ananjeva, N.B.; Larson, A.; Rastegar-Pouyani, N.; Shammakov, S.M.; Papenfuss, T.J.

Mol. Phylogenet. Evol. 10, 118-131, 1998

A;Title: Phylogenetic relationships among agamid lizards of the *Laudakia caucasia* species group: Testing hypotheses of biogeographic fragmentation and an area cladogram for the Iranian Plateau.

A;Reference number: Z17470; MUID:98424476; PMID:9751922

A;Accession: T12244

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC>

A;Cross-references: EMBL:AF028677; NID:g3641444; PID:g3641447; PIDN:AAC99584.1

A;Experimental source: specimen voucher CAS183009; California Academy of Sciences, San Francisco

C;Genetics:

A;Gene: COI
A;Genome: mitochondrion
C;Keywords: mitochondrion; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 5 TR 6

RESULT 42

T12248

cytochrome-c oxidase (EC 1.9.3.1) chain I - *Laudakia microlepis* mitochondrion (fragment)

C;Species: mitochondrion *Laudakia microlepis*

C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 03-Aug-2001

C;Accession: T12248

R;Macey, J.R.; Schulte II, J.A.; Ananjeva, N.B.; Larson, A.; Rastegar-Pouyani, N.; Shammakov, S.M.; Papenfuss, T.J.

Mol. Phylogenet. Evol. 10, 118-131, 1998

A;Title: Phylogenetic relationships among agamid lizards of the *Laudakia caucasia* species group: Testing hypotheses of biogeographic fragmentation and an area cladogram for the Iranian Plateau.

A;Reference number: Z17470; MUID:98424476; PMID:9751922

A;Accession: T12248

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC>

A;Cross-references: EMBL:AF028678; NID:g3641448; PID:g3641451; PIDN:AAC99587.1

A;Experimental source: specimen voucher GNM. RE. ex.-P120; Goteborg Natural History Museum Reptilia Exotica, Goteborg, Sweden

C;Genetics:

A;Gene: COI

A;Genome: mitochondrion

C;Keywords: mitochondrion; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 5 TR 6

RESULT 43

A48973

glucoamylase A1 (EC 3.2.1.-) - *Chalara paradoxa* (fragment)

C;Species: *Chalara paradoxa*

C;Date: 19-Dec-1993 #sequence_revision 25-Apr-1997 #text_change 25-Apr-1997

C;Accession: A48973

R;Monma, M.; Kainuma, K.

Carbohydr. Res. 227, 385-388, 1992

A;Title: Heterogeneity of the glucoamylase components of the raw-starch-digesting amylase from *Chalara paradoxa*.

A;Reference number: A48973; MUID:92361881; PMID:1499035

A;Accession: A48973

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <MON>

A;Note: sequence extracted from NCBI backbone (NCBIP:110946)

C;Keywords: glycosidase; hydrolase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ER 7
||
Db 10 ER 11

RESULT 44

S60294

tubulin 2 beta-3 chain - fruit fly (*Drosophila melanogaster*) (fragment)

C;Species: *Drosophila melanogaster*

C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jun-2002

C;Accession: S60294

R;Chapel, S.; Sobrier, M.L.; Montpied, P.; Micard, D.; Bruhat, A.; Couderc, J.L.; Dastugue, B.

Insect Mol. Biol. 2, 39-48, 1993

A;Title: In *Drosophila* Kc cells 20-OHE induction of the 60C beta-3 tubulin gene expression is a primary transcriptional event.

A;Reference number: S60292; MUID:97242543; PMID:9087542

A;Accession: S60294

A;Molecule type: mRNA

A;Residues: 1-11 <CHA>

A;Cross-references: EMBL:X60393

C;Genetics:

A;Gene: FlyBase:beta-Tub60D

A;Cross-references: FlyBase:FBgn0003888

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 5 TR 6

RESULT 45

PC2124

aminotransferase chimera DY376 - synthetic (fragment)

C;Species: synthetic

C;Date: 28-May-1999 #sequence_revision 28-May-1999 #text_change 28-May-1999

C;Accession: PC2124

R;Miyazawa, K.; Kawaguchi, S.; Okamoto, A.; Kato, R.; Ogawa, T.; Kuramitsu, S.
J. Biochem. 115, 568-577, 1994

A;Title: Construction of aminotransferase chimeras and analysis of their substrate specificity.
A;Reference number: JX0315; MUID:94334304; PMID:8056774
A;Accession: PC2124
A;Molecule type: DNA
A;Residues: 1-11 <MIY>
C;Comment: This is a chimeric enzyme of Escherichia coli aspartate aminotransferase (EC 2.6.1.1) and aromatic amino acid aminotransferase (EC 2.6.1.57).
C;Comment: The parental enzymes catalyze the reversible amino group transfer reaction between L-aspartate and L-glutamate, respectively.
C;Genetics:
A;Gene: aspC; tyrB
C;Keywords: aminotransferase

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RE 6
||
Db 4 RE 5

RESULT 46

XAVIBH

bradykinin-potentiating peptide - halys viper

N;Alternate names: BPP

C;Species: Agkistrodon halys (halys viper)

C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 05-Aug-1994

C;Accession: JC0002

R;Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.

Peptides 6, 339-342, 1985

A;Title: Structure-function studies on the bradykinin potentiating peptide from Chinese snake venom (Agkistrodon halys Pallas).

A;Reference number: JC0002; MUID:86177022; PMID:3008123

A;Accession: JC0002

A;Molecule type: protein

A;Residues: 1-11 <CHI>

C;Comment: Because this peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin, it is an antihypertensive agent.

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; antihypertensive; bradykinin; pyroglutamic acid; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 3 R 3

RESULT 47

XASNBA

bradykinin-potentiating peptide B - mamushi

C;Species: Agkistrodon blomhoffi (mamushi)

C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995

C;Accession: A01254

R;Kato, H.; Suzuki, T.

Proc. Jpn. Acad. 46, 176-181, 1970

A;Reference number: A01254

A;Accession: A01254

A;Molecule type: protein

A;Residues: 1-11 <KAT>

A;Note: the sequence of the natural peptide was confirmed by the synthesis and analysis of a peptide having the identical structure and biological properties

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2

|

Db 6 R 6

RESULT 48

ECLQ2M

tachykinin II - migratory locust

C;Species: Locusta migratoria (migratory locust)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Dec-1995

C;Accession: S08266

R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; de Loof, A.

FEBS Lett. 261, 397-401, 1990

A;Title: Locustatachykinin I and II, two novel insect neuropeptides with homology to peptides of the vertebrate tachykinin family.

A;Reference number: S08265; MUID:90184489; PMID:2311766

A;Accession: S08266

A;Molecule type: protein

A;Residues: 1-11 <SCH>

C;Superfamily: tachykinin

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;11/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1

|

Db 1 A 1

RESULT 49

SPHO

substance P - horse

C;Species: Equus caballus (domestic horse)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 23-Aug-1996
C;Accession: A01558
R;Studer, R.O.; Trzeciak, A.; Lergier, W.
Helv. Chim. Acta 56, 860-866, 1973
A;Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pferdedarm.
A;Reference number: A01558
A;Accession: A01558
A;Molecule type: protein
A;Residues: 1-11 <STU>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; hormone
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 1 R 1

RESULT 50

A60654
substance P - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 08-Dec-1995
C;Accession: A60654
R;Murphy, R.
Neuropeptides 14, 105-110, 1989
A;Title: Primary amino acid sequence of guinea-pig substance P.
A;Reference number: A60654; MUID:90044685; PMID:2478925
A;Accession: A60654
A;Molecule type: protein
A;Residues: 1-11 <MUR>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 1 R 1

RESULT 51

GMROL
leucosulfakinin - Madeira cockroach
N;Alternate names: LSK
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 13-Sep-1996
C;Accession: A01622
R;Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.

Science 234, 71-73, 1986

A;Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and cholecystokinin.

A;Reference number: A01622; MUID:86315858; PMID:3749893

A;Accession: A01622

A;Molecule type: protein

A;Residues: 1-11 <NAC>

C;Superfamily: gastrin

C;Keywords: amidated carboxyl end; hormone; sulfoprotein

F;6/Binding site: sulfate (Tyr) (covalent) #status experimental

F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 E 6
|
Db 1 E 1

RESULT 52

LFTWWE

probable trpEG leader peptide - *Thermus aquaticus*

C;Species: *Thermus aquaticus*

C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999

C;Accession: S03315

R;Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.

Biochim. Biophys. Acta 950, 303-312, 1988

A;Title: Molecular cloning and nucleotide sequence of *Thermus thermophilus* HB8 trpE and trpG.

A;Reference number: S03315; MUID:89000781; PMID:2844259

A;Accession: S03315

A;Molecule type: DNA

A;Residues: 1-11 <SAT>

A;Cross-references: EMBL:X07744; NID:g48261; PIDN:CAA30565.1; PID:g48262

A;Note: the source is designated as *Thermus thermophilus* HB8

C;Genetics:

A;Gene: trpL

C;Superfamily: probable trpEG leader peptide

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 2 A 2

RESULT 53

S66196

alcohol dehydrogenase (EC 1.1.1.1) class III high affinity form - cod (*Gadus* sp.) (fragment)

C;Species: *Gadus* sp. (cod)

C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 12-Jun-1998

C;Accession: S66196

R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.;
Hendrickson, R.C.; Michel, H.; Shabanowitz, J.; Hunt, D.F.; Joernvall, H.
FEBS Lett. 367, 237-240, 1995
A;Title: Multiplicity of N-terminal structures of medium-chain alcohol
dehydrogenases. Mass-spectrometric analysis of plant, lower vertebrate and
higher vertebrate class I, II, and III forms of the enzyme.
A;Reference number: S66191; MUID:95331382; PMID:7607314
A;Accession: S66196
A;Molecule type: protein
A;Residues: 1-11 <HJE>
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 T 4
|
Db 1 T 1

RESULT 54

G42762

proteasome endopeptidase complex (EC 3.4.25.1) subunit 13 - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Feb-2003
C;Accession: G42762
R;Dick, L.R.; Moomaw, C.R.; Pramanik, B.C.; DeMartino, G.N.; Slaughter, C.A.
Biochemistry 31, 7347-7355, 1992
A;Title: Identification and localization of a cysteinyl residue critical for the
trypsin-like catalytic activity of the proteasome.
A;Reference number: A42762; MUID:92378961; PMID:1510924
A;Accession: G42762
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <DIC>
A;Note: sequence extracted from NCBI backbone (NCBIP:112176)
C;Superfamily: multicatalytic endopeptidase complex chain C9
C;Keywords: hydrolase

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 T 4
|
Db 3 T 3

RESULT 55

S68392

H+-transporting two-sector ATPase (EC 3.6.3.14) chain I - Chlamydomonas
reinhardtii chloroplast (fragment)
N;Alternate names: ATP synthase chain I
C;Species: chloroplast Chlamydomonas reinhardtii
C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 03-Jun-2002

C;Accession: S68392
 R;Fiedler, H.R.; Schmid, R.; Leu, S.; Shavit, N.; Strotmann, H.
 FEBS Lett. 377, 163-166, 1995
 A;Title: Isolation of CF(0)CF(1) from Chlamydomonas reinhardtii cw15 and the N-terminal amino acid sequences of the CF(0)CF(1) subunits.
 A;Reference number: S68388; MUID:96128220; PMID:8543042
 A;Accession: S68392
 A;Molecule type: protein
 A;Residues: 1-11 <FIE>
 A;Experimental source: strain CW15
 C;Genetics:
 A;Genome: chloroplast
 C;Superfamily: H⁺-transporting ATP synthase protein 6
 C;Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; thylakoid

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 E 6
 |
 Db 1 E 1

RESULT 56

A33917
 dihydroorotase (EC 3.5.2.3) - Chinese hamster (fragment)
 C;Species: Cricetulus griseus (Chinese hamster)
 C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 07-Nov-1997
 C;Accession: A33917
 R;Simmer, J.P.; Kelly, R.E.; Scully, J.L.; Grayson, D.R.; Rinker Jr., A.G.; Bergh, S.T.; Evans, D.R.
 Proc. Natl. Acad. Sci. U.S.A. 86, 4382-4386, 1989
 A;Title: Mammalian aspartate transcarbamylase (ATCase): sequence of the ATCase domain and interdomain linker in the CAD multifunctional polypeptide and properties of the isolated domain.
 A;Reference number: A33917; MUID:89282776; PMID:2543974
 A;Accession: A33917
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-11 <SIM>
 A;Cross-references: GB:M23652
 C;Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology; Bacillus dihydroorotase homology; biotin carboxylase homology; carbamoyl-phosphate synthase (ammonia) homology; carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology; carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology; trpG homology
 C;Keywords: hydrolase

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 E 6
 |
 Db 2 E 2

RESULT 57

B49164

chromogranin-B - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997

C;Accession: B49164

R;Nielsen, E.; Welinder, B.S.; Madsen, O.D.

Endocrinology 129, 3147-3156, 1991

A;Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides through processing at mono-, di-, or tribasic residues.

A;Reference number: A49164; MUID:92063871; PMID:1954895

A;Accession: B49164

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <NIE>

A;Note: sequence extracted from NCBI backbone (NCBIP:66370)

C;Superfamily: chromogranin B precursor

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 S 9

|

Db 3 S 3

RESULT 58

JN0023

substance P - chicken

C;Species: Gallus gallus (chicken)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jul-1997

C;Accession: JN0023

R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.

Regul. Pept. 20, 171-180, 1988

A;Title: [Arg3]substance P and neurokinin A from chicken small intestine.

A;Reference number: JN0023; MUID:88204263; PMID:2452461

A;Accession: JN0023

A;Molecule type: protein

A;Residues: 1-11 <CON>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2

|

Db 1 R 1

RESULT 59

A38841

rhodopsin homolog - squid (*Watasenia scintillans*) (fragment)
 N;Alternate names: visual pigment protein
 C;Species: *Watasenia scintillans* (sparkling enope)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 31-Oct-1997
 C;Accession: A38841
 R;Seidou, M.; Kubota, I.; Hiraki, K.; Kito, Y.
 Biochim. Biophys. Acta 957, 318-321, 1988
 A;Title: Amino acid sequence of the retinal binding site of squid visual pigment.
 A;Reference number: PT0063; MUID:89051045; PMID:3191148
 A;Accession: A38841
 A;Molecule type: protein
 A;Residues: 1-11 <SEI>
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: chromoprotein; retinal
 F;3/Binding site: retinal (Lys) (covalent) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 2 A 2

RESULT 60

PQ0682

photosystem I 17.5K D2 chain - common tobacco (fragment)

C;Species: *Nicotiana tabacum* (common tobacco)

C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999

C;Accession: PQ0682

R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.

Plant Physiol. 102, 1259-1267, 1993

A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH and psaL are all present in isoforms in *Nicotiana* spp.

A;Reference number: PQ0667; MUID:94105345; PMID:8278548

A;Accession: PQ0682

A;Molecule type: protein

A;Residues: 1-11 <OBO>

C;Superfamily: photosystem I chain II

C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 1 A 1

RESULT 61

S00616

parasporal crystal protein, wax moth-specific - *Bacillus thuringiensis* (strain galleriae 11-67) (fragment)

N;Alternate names: delta-endotoxin; parasporal crystal protein positive chain

C;Species: *Bacillus thuringiensis*
 C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 13-Sep-1996
 C;Accession: S00616
 R;Chestukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M.
 FEBS Lett. 232, 249-251, 1988
 A;Title: *Bacillus thuringiensis* ssp. *galleriae* simultaneously produces two
 delta-endotoxins differing strongly in primary structure and entomocidal
 activity.
 A;Reference number: S00615
 A;Accession: S00616
 A;Molecule type: protein
 A;Residues: 1-11 <CHE>
 C;Comment: This toxin is effective against the larvae of *Galleria melonella*
 (greater wax moth) but not those of *Lymantria dispar* (gypsy moth).
 C;Superfamily: parasporal crystal protein
 C;Keywords: delta-endotoxin

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 4 A 4

RESULT 62
 C53652

rhlR protein - *Pseudomonas aeruginosa* (fragment)
 C;Species: *Pseudomonas aeruginosa*
 C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 21-Aug-1998
 C;Accession: C53652
 R;Ochsner, U.A.; Fiechter, A.; Reiser, J.
 J. Biol. Chem. 269, 19787-19795, 1994
 A;Title: Isolation, characterization, and expression in *Escherichia coli* of the
Pseudomonas aeruginosa rhlAB genes encoding a rhamnosyltransferase involved in
 rhamnolipid biosurfactant synthesis.
 A;Reference number: A53652; MUID:94327521; PMID:8051059
 A;Accession: C53652
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-11 <OCH>
 A;Cross-references: GB:L28170
 C;Superfamily: sdiA regulatory protein

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
 |
 Db 2 R 2

RESULT 63
 S09074
 cytochrome P450-4b - rat (fragment)

N;Alternate names: cytochrome P450K-5
 N;Contains: oxidoreductase (EC 1.-.-.-)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 05-Mar-1999
 C;Accession: S09074
 R;Imaoka, S.; Terano, Y.; Funae, Y.
 Arch. Biochem. Biophys. 278, 168-178, 1990
 A;Title: Changes in the amount of cytochrome P450s in rat hepatic microsomes with starvation.
 A;Reference number: S09072; MUID:90210577; PMID:2321956
 A;Accession: S09074
 A;Molecule type: protein
 A;Residues: 1-11 <IMA>
 C;Superfamily: unassigned cytochrome P450; cytochrome P450 homology
 C;Keywords: heme; microsome; monooxygenase; oxidoreductase; transmembrane protein

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 T 4
 |
 Db 5 T 5

RESULT 64

A57458
 gene Gax protein - mouse (fragment)
 C;Species: Mus sp. (mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 15-Oct-1999
 C;Accession: A57458
 R;Andres, V.; Fisher, S.; Wearsch, P.; Walsh, K.
 Mol. Cell. Biol. 15, 4272-4281, 1995
 A;Title: Regulation of Gax homeobox gene transcription by a combination of positive factors including myocyte-specific enhancer factor 2.
 A;Reference number: A57458; MUID:95349593; PMID:7623821
 A;Accession: A57458
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-11 <RES>
 A;Cross-references: GB:S79168; NID:g1050991
 C;Genetics:
 A;Gene: Gax
 C;Superfamily: unassigned homeobox proteins; homeobox homology
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 E 6
 |
 Db 2 E 2

RESULT 65

D60409

kassinin-like peptide K-III - frog (*Pseudophryne guentheri*)

C;Species: *Pseudophryne guentheri*

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000

C;Accession: D60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog *Pseudophryne guentheri*.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: D60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 E 6
|
Db 6 E 6

RESULT 66

F60409

substance P-like peptide II - frog (*Pseudophryne guentheri*)

C;Species: *Pseudophryne guentheri*

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000

C;Accession: F60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog *Pseudophryne guentheri*.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: F60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 E 6
|
Db 6 E 6

RESULT 67

E60409

substance P-like peptide I - frog (*Pseudophryne guentheri*)

C;Species: *Pseudophryne guentheri*

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000

C;Accession: E60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog *Pseudophryne guentheri*.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: E60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
|
Db 5 D 5

RESULT 68

A61365

phyllokinin - Rohde's leaf frog

N;Alternate names: bradykinyl-isoleucyl-tyrosine O-sulfate

C;Species: *Phyllomedusa rohdei* (Rohde's leaf frog)

C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000

C;Accession: A61365

R;Anastasi, A.; Bertaccini, G.; Erspamer, V.

Br. J. Pharmacol. 27, 479-485, 1966

A;Title: Pharmacological data on phyllokinin (bradykinyl-isoleucyl-tyrosine O-sulphate) and bradykinyl-isoleucyl-tyrosine.

A;Reference number: A61365; MUID:67179312; PMID:5970899

A;Accession: A61365

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: unassigned animal peptides

C;Keywords: sulfoprotein

F;11/Binding site: sulfate (Tyr) (covalent) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 1 R 1

RESULT 69

S23308

substance P - rainbow trout

C;Species: Oncorhynchus mykiss (rainbow trout)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000

C;Accession: S23308

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23308

A;Molecule type: protein

A;Residues: 1-11 <JEN>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Superfamily: unassigned animal peptides

C;Keywords: neuropeptide; amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match	9.18;	Score 1;	DB 2;	Length 11;
Best Local Similarity	100.08;	Pred. No. 2e+05;		
Matches	1;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3

|

Db 1 K 1

RESULT 70

S23306

substance P - Atlantic cod

C;Species: Gadus morhua (Atlantic cod)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000

C;Accession: S23306

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23306

A;Molecule type: protein

A;Residues: 1-11 <JEN>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Superfamily: unassigned animal peptides

C;Keywords: neuropeptide; amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
|
Db 1 K 1

RESULT 71

B60409

kassinin-like peptide K-I - frog (*Pseudophryne guentheri*)

C;Species: *Pseudophryne guentheri*

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000

C;Accession: B60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;
Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of
the Australian frog *Pseudophryne guentheri*.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: B60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

A;Note: this peptide was also found in a deamidated form

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
|
Db 5 D 5

RESULT 72

C60409

kassinin-like peptide K-II - frog (*Pseudophryne guentheri*)

C;Species: *Pseudophryne guentheri*

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000

C;Accession: C60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;
Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of
the Australian frog *Pseudophryne guentheri*.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: C60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

A;Note: this peptide was also found in a deamidated form

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
|
Db 5 D 5

RESULT 73

S07203

uperolein - frog (*Uperoleia marmorata*)

C;Species: *Uperoleia marmorata*

C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000

C;Accession: S07203

R;Anastasi, A.; Erspamer, V.; Endean, R.

Experientia 31, 394-395, 1975

A;Title: Structure of uperolein, a physalaemin-like endecapeptide occurring in the skin of *Uperoleia rugosa* and *Uperoleia marmorata*.

A;Reference number: S07203; MUID:75131227; PMID:1120493

A;Accession: S07203

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
|
Db 3 D 3

RESULT 74

S07207

Crinia-angiotensin, skin - frog (*Crinia georgiana*)

C;Species: *Crinia georgiana*

C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Aug-2000

C;Accession: S07207

R;Erspamer, V.; Melchiorri, P.; Nakajima, T.; Yasuhara, T.; Endean, R.

Experientia 35, 1132-1133, 1979

A;Title: Amino acid composition and sequence of crinia-angiotensin, an angiotensin II-like endecapeptide from the skin of the Australian frog *Crinia georgiana*.

A;Reference number: S07207; MUID:80024575; PMID:488254

A;Accession: S07207

A;Molecule type: protein

A;Residues: 1-11 <ERS>

C;Superfamily: unassigned animal peptides

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 A 1

RESULT 75

S07201

physalaemin - frog (*Physalaemus fuscumaculatus*)

C;Species: *Physalaemus fuscumaculatus*

C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000

C;Accession: S07201

R;Erspamer, V.; Anastasi, A.; Bertaccini, G.; Cei, J.M.

Experientia 20, 489-490, 1964

A;Title: Structure and pharmacological actions of physalaemin, the main active polypeptide of the skin of *Physalaemus fuscumaculatus*.

A;Reference number: S07201; MUID:66076612; PMID:5857249

A;Accession: S07201

A;Molecule type: protein

A;Residues: 1-11 <ERS>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 2 A 2

Search completed: April 8, 2004, 15:49:26

Job time : 8.61538 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:47:33 ; Search time 30.3077 Seconds
(without alignments)
95.432 Million cell updates/sec

Title: US-09-787-443A-14
Perfect score: 11
Sequence: 1 ARKTRERKSKD 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1073127 seqs, 262937947 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9223

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result
No. Score Match Length DB ID Description

1	4	36.4	11	9	US-09-966-871-3	Sequence 3, Appli
2	4	36.4	11	10	US-09-876-904A-239	Sequence 239, App
3	4	36.4	11	12	US-10-458-860-3	Sequence 3, Appli
4	4	36.4	11	12	US-09-727-739B-18	Sequence 18, Appl
5	4	36.4	11	13	US-10-039-645-3	Sequence 3, Appli
6	4	36.4	11	14	US-10-139-084-3	Sequence 3, Appli
7	3	27.3	11	9	US-09-839-666-12	Sequence 12, Appl
8	3	27.3	11	9	US-09-941-611-3	Sequence 3, Appli
9	3	27.3	11	9	US-09-949-196-16	Sequence 16, Appl
10	3	27.3	11	9	US-09-071-838-212	Sequence 212, App
11	3	27.3	11	9	US-09-071-838-253	Sequence 253, App
12	3	27.3	11	10	US-09-882-291-44	Sequence 44, Appl
13	3	27.3	11	10	US-09-775-052-3	Sequence 3, Appli
14	3	27.3	11	10	US-09-847-946A-126	Sequence 126, App
15	3	27.3	11	10	US-09-847-946A-127	Sequence 127, App
16	3	27.3	11	10	US-09-876-904A-33	Sequence 33, Appl
17	3	27.3	11	10	US-09-876-904A-202	Sequence 202, App
18	3	27.3	11	10	US-09-876-904A-236	Sequence 236, App
19	3	27.3	11	10	US-09-876-904A-237	Sequence 237, App
20	3	27.3	11	10	US-09-876-904A-509	Sequence 509, App
21	3	27.3	11	10	US-09-876-904A-555	Sequence 555, App
22	3	27.3	11	10	US-09-992-665-55	Sequence 55, Appl
23	3	27.3	11	10	US-09-972-656-6	Sequence 6, Appli
24	3	27.3	11	10	US-09-829-922-4	Sequence 4, Appli
25	3	27.3	11	10	US-09-829-922-13	Sequence 13, Appl
26	3	27.3	11	10	US-09-940-316B-57	Sequence 57, Appl
27	3	27.3	11	12	US-10-430-685-39	Sequence 39, Appl
28	3	27.3	11	12	US-10-462-452-276	Sequence 276, App
29	3	27.3	11	12	US-10-462-452-292	Sequence 292, App
30	3	27.3	11	12	US-10-462-452-308	Sequence 308, App
31	3	27.3	11	12	US-10-462-452-324	Sequence 324, App
32	3	27.3	11	12	US-10-462-452-340	Sequence 340, App
33	3	27.3	11	12	US-10-462-452-356	Sequence 356, App
34	3	27.3	11	12	US-10-462-452-372	Sequence 372, App
35	3	27.3	11	12	US-10-462-452-388	Sequence 388, App
36	3	27.3	11	12	US-10-398-104-203	Sequence 203, App
37	3	27.3	11	12	US-10-344-878-5	Sequence 5, Appli
38	3	27.3	11	12	US-10-344-878-6	Sequence 6, Appli
39	3	27.3	11	12	US-09-822-965-16	Sequence 16, Appl
40	3	27.3	11	12	US-09-823-418-16	Sequence 16, Appl
41	3	27.3	11	13	US-10-044-034-14	Sequence 14, Appl
42	3	27.3	11	14	US-10-124-880-30	Sequence 30, Appl
43	3	27.3	11	14	US-10-062-710-165	Sequence 165, App
44	3	27.3	11	14	US-10-062-710-166	Sequence 166, App
45	3	27.3	11	14	US-10-044-995-3	Sequence 3, Appli
46	3	27.3	11	14	US-10-229-915-21	Sequence 21, Appl
47	3	27.3	11	14	US-10-211-088-202	Sequence 202, App
48	3	27.3	11	14	US-10-136-738-2	Sequence 2, Appli
49	3	27.3	11	14	US-10-213-512-212	Sequence 212, App
50	3	27.3	11	14	US-10-213-512-253	Sequence 253, App
51	3	27.3	11	14	US-10-197-954-48	Sequence 48, Appl
52	3	27.3	11	14	US-10-160-290-4	Sequence 4, Appli
53	3	27.3	11	14	US-10-160-290-13	Sequence 13, Appl
54	3	27.3	11	14	US-10-234-579-12	Sequence 12, Appl
55	3	27.3	11	14	US-10-195-730-318	Sequence 318, App
56	3	27.3	11	14	US-10-032-201B-310	Sequence 310, App

57	3	27.3	11	14	US-10-224-999A-2198	Sequence 2198, Ap
58	3	27.3	11	14	US-10-224-999A-2199	Sequence 2199, Ap
59	3	27.3	11	14	US-10-224-999A-2200	Sequence 2200, Ap
60	3	27.3	11	14	US-10-224-999A-2201	Sequence 2201, Ap
61	3	27.3	11	14	US-10-224-999A-2202	Sequence 2202, Ap
62	3	27.3	11	14	US-10-168-445-83	Sequence 83, Appl
63	3	27.3	11	14	US-10-105-232-108	Sequence 108, App
64	3	27.3	11	14	US-10-161-791-283	Sequence 283, App
65	3	27.3	11	14	US-10-405-339-13	Sequence 13, Appl
66	3	27.3	11	14	US-10-189-437-95	Sequence 95, Appl
67	3	27.3	11	15	US-10-411-869A-30	Sequence 30, Appl
68	3	27.3	11	15	US-10-378-173-136	Sequence 136, App
69	3	27.3	11	15	US-10-014-099F-30	Sequence 30, Appl
70	3	27.3	11	16	US-10-443-622-90	Sequence 90, Appl
71	2	18.2	11	8	US-08-996-470-2	Sequence 2, Appli
72	2	18.2	11	8	US-08-424-550B-223	Sequence 223, App
73	2	18.2	11	8	US-08-424-550B-523	Sequence 523, App
74	2	18.2	11	8	US-08-424-550B-550	Sequence 550, App
75	2	18.2	11	8	US-08-809-423A-5	Sequence 5, Appli
76	2	18.2	11	8	US-08-811-519A-12	Sequence 12, Appl
77	2	18.2	11	8	US-08-765-837-15	Sequence 15, Appl
78	2	18.2	11	8	US-08-344-824-24	Sequence 24, Appl
79	2	18.2	11	8	US-08-344-824-44	Sequence 44, Appl
80	2	18.2	11	9	US-09-222-179-1	Sequence 1, Appli
81	2	18.2	11	9	US-09-113-924-18	Sequence 18, Appl
82	2	18.2	11	9	US-09-113-924-22	Sequence 22, Appl
83	2	18.2	11	9	US-09-748-062-28	Sequence 28, Appl
84	2	18.2	11	9	US-09-205-658-302	Sequence 302, App
85	2	18.2	11	9	US-09-291-809C-9	Sequence 9, Appli
86	2	18.2	11	9	US-09-291-809C-13	Sequence 13, Appl
87	2	18.2	11	9	US-09-850-373-1	Sequence 1, Appli
88	2	18.2	11	9	US-09-828-592-7	Sequence 7, Appli
89	2	18.2	11	9	US-09-828-592-9	Sequence 9, Appli
90	2	18.2	11	9	US-09-828-592-12	Sequence 12, Appl
91	2	18.2	11	9	US-09-765-527-153	Sequence 153, App
92	2	18.2	11	9	US-09-780-070-25	Sequence 25, Appl
93	2	18.2	11	9	US-09-780-070-37	Sequence 37, Appl
94	2	18.2	11	9	US-09-788-626-39	Sequence 39, Appl
95	2	18.2	11	9	US-09-815-108-9	Sequence 9, Appli
96	2	18.2	11	9	US-09-010-714-6	Sequence 6, Appli
97	2	18.2	11	9	US-09-823-649A-6	Sequence 6, Appli
98	2	18.2	11	9	US-09-823-649A-7	Sequence 7, Appli
99	2	18.2	11	9	US-09-823-649A-17	Sequence 17, Appl
100	2	18.2	11	9	US-09-823-649A-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1

US-09-966-871-3

; Sequence 3, Application US/09966871

; Patent No. US20020127539A1

; GENERAL INFORMATION:

; APPLICANT: Kopin, Alan S.

; TITLE OF INVENTION: Assays for Identifying Receptors Having

; TITLE OF INVENTION: Alterations in Signaling

```
; FILE REFERENCE: 00398/512002
; CURRENT APPLICATION NUMBER: US/09/966,871
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,302
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/288,644
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-871-3
```

```
Query Match          36.4%; Score 4; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      5 RERK 8
        ||||
Db      1 RERK 4
```

RESULT 2

```
US-09-876-904A-239
; Sequence 239, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 239
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Hydrophilic protein
US-09-876-904A-239
```

```
Query Match          36.4%; Score 4; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      5 RERK 8
        ||||
Db      8 RERK 11
```

RESULT 3

US-10-458-860-3

```
; Sequence 3, Application US/10458860
; Publication No. US20040049800A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: Rapid Methods For Assessing Therapeutic
; TITLE OF INVENTION: Activity Using Animals Expressing Constitutively Active
G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: 00398/517002
; CURRENT APPLICATION NUMBER: US/10/458,860
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: US 60/388,450
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic fragment
US-10-458-860-3
```

```
Query Match          36.4%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      5 RERK 8
        ||||
Db      1 RERK 4
```

RESULT 4

US-09-727-739B-18

```
; Sequence 18, Application US/09727739B
; Publication No. US20010025097A1
; GENERAL INFORMATION:
; APPLICANT: Sheridan, Mark
; APPLICANT: Kittilson, Jeffrey
; APPLICANT: Moore, Craig
; TITLE OF INVENTION: Somatostatins and Methods
; FILE REFERENCE: 255.00040101
; CURRENT APPLICATION NUMBER: US/09/727,739B
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/168,934
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Oncorhynchus mykiss
```

US-09-727-739B-18

Query Match 36.4%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RERK 8
||||
Db 8 RERK 11

RESULT 5

US-10-039-645-3
; Sequence 3, Application US/10039645
; Publication No. US20020147170A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: Constitutively Active, Hypersensitive,
; TITLE OF INVENTION: and No. US20020147170A1functional Receptors as No.
US20020147170A1 Therapeutic Agents
; FILE REFERENCE: 00398/510002
; CURRENT APPLICATION NUMBER: US/10/039,645
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,550
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-645-3

Query Match 36.4%; Score 4; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RERK 8
||||
Db 1 RERK 4

RESULT 6

US-10-139-084-3
; Sequence 3, Application US/10139084
; Publication No. US20030087313A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: Dose Response-Based Methods For
; TITLE OF INVENTION: Identifying Receptors Having Alterations in Signaling
; FILE REFERENCE: 00398/515002
; CURRENT APPLICATION NUMBER: US/10/139,084
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/288,647
; PRIOR FILING DATE: 2001-05-03

; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-084-3

Query Match 36.4%; Score 4; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RERK 8
||||
Db 1 RERK 4

RESULT 7

US-09-839-666-12

; Sequence 12, Application US/09839666
; Patent No. US20020025513A1
; GENERAL INFORMATION:
; APPLICANT: SALLBERG, MATTI
; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
; EXCHANGER
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DARBY & DARBY PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/839,666
; FILING DATE: 19-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/737,085
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 3846/0C569
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7659
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-839-666-12

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKT 4
|||
Db 2 RKT 4

RESULT 8

US-09-941-611-3

; Sequence 3, Application US/09941611
; Patent No. US20020106640A1
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT J
; POLLET, DIRK
; MAERTENS, GEERT
; VAN HEUVERSWUN, HUGO
; TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF
; ANTIBODIES TO HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/941,611
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/391,671
; FILING DATE: 1995-02-21
; APPLICATION NUMBER: WO PCT/EP91/02409
; FILING DATE: 13-DEC-1991
; APPLICATION NUMBER: EP 90124241.2
; FILING DATE: 14-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-941-611-3

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKT 4
|||
Db 2 RKT 4

RESULT 9
US-09-949-196-16
; Sequence 16, Application US/09949196
; Patent No. US20020147145A1
; GENERAL INFORMATION:
; APPLICANT: Zealand Pharmaceuticals A/S
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THE DEGRADATION OF
Cdc25A IN RESPONSE
; TITLE OF INVENTION: TO DNA DAMAGE
; FILE REFERENCE: 55888 (45487)
; CURRENT APPLICATION NUMBER: US/09/949,196
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
sequence
US-09-949-196-16

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 2 ARK 4

RESULT 10
US-09-071-838-212
; Sequence 212, Application US/09071838
; Patent No. US20020152501A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.

; APPLICANT: Ohad, Nir
 ; APPLICANT: Kiyosue, Tomohiro
 ; APPLICANT: Yadegari, Ramin
 ; APPLICANT: Margossian, Linda
 ; APPLICANT: Harada, John
 ; APPLICANT: Goldberg, Robert B.
 ; TITLE OF INVENTION: Nucleic Acids That Control Seed and
 ; TITLE OF INVENTION: Fruit Development in Plants
 ; NUMBER OF SEQUENCES: 324
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/071,838
 ; FILING DATE: 01-MAY-1998
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bastian, Kevin L.
 ; REGISTRATION NUMBER: 34,774
 ; REFERENCE/DOCKET NUMBER: 023070-086100US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 212:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-09-071-838-212

Query Match 27.3%; Score 3; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKS 9
 |||
 Db 2 RKS 4

RESULT 11
 US-09-071-838-253
 ; Sequence 253, Application US/09071838
 ; Patent No. US20020152501A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fischer, Robert L.
 ; APPLICANT: Ohad, Nir
 ; APPLICANT: Kiyosue, Tomohiro

; APPLICANT: Yadegari, Ramin
 ; APPLICANT: Margossian, Linda
 ; APPLICANT: Harada, John
 ; APPLICANT: Goldberg, Robert B.
 ; TITLE OF INVENTION: Nucleic Acids That Control Seed and
 ; TITLE OF INVENTION: Fruit Development in Plants
 ; NUMBER OF SEQUENCES: 324
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/071,838
 ; FILING DATE: 01-MAY-1998
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bastian, Kevin L.
 ; REGISTRATION NUMBER: 34,774
 ; REFERENCE/DOCKET NUMBER: 023070-086100US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 253:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-09-071-838-253

Query Match 27.3%; Score 3; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ERK 8
 |||
 Db 5 ERK 7

RESULT 12
 US-09-882-291-44
 ; Sequence 44, Application US/09882291
 ; Publication No. US20030040472A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zealand Pharmaceuticals A/S
 ; TITLE OF INVENTION: No. US20030040472A1el Peptide Conjugates
 ; FILE REFERENCE: 007-2001
 ; CURRENT APPLICATION NUMBER: US/09/882,291
 ; CURRENT FILING DATE: 2001-06-15

```

*
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
sequence
US-09-882-291-44

```

```

Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 ARK 3
        |||
Db      2 ARK 4

```

RESULT 13

```

US-09-775-052-3
; Sequence 3, Application US/09775052
; Publication No. US20030054000A1
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48881/1742
; CURRENT APPLICATION NUMBER: US/09/775,052
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 09/208,966
; PRIOR FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: 60/082,402
; PRIOR FILING DATE: 1998-04-20
; PRIOR APPLICATION NUMBER: 60/069,012
; PRIOR FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human
US-09-775-052-3

```

```

Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 ARK 3
        |||
Db      2 ARK 4

```

RESULT 14

```

US-09-847-946A-126
; Sequence 126, Application US/09847946A
; Publication No. US20030054999A1

```

```

; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 126
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:membrane
; OTHER INFORMATION: translocation domain
US-09-847-946A-126

```

```

Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 ARK 3
        |||
Db      2 ARK 4

```

```

RESULT 15
US-09-847-946A-127
; Sequence 127, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 127
; LENGTH: 11
; TYPE: PRT

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:membrane
; OTHER INFORMATION: translocation domain
US-09-847-946A-127

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 2 ARK 4

RESULT 16

US-09-876-904A-33

; Sequence 33, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Polyma
virus
; OTHER INFORMATION: major capsid protein VP1
US-09-876-904A-33

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKS 9
|||
Db 4 RKS 6

RESULT 17

US-09-876-904A-202

; Sequence 202, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
 THERAPEUTIC
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
 PEPTIDE
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
 ; FILE REFERENCE: TB-2002.00
 ; CURRENT APPLICATION NUMBER: US/09/876,904A
 ; CURRENT FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: US 60/210,925
 ; PRIOR FILING DATE: 2000-06-09
 ; NUMBER OF SEQ ID NOS: 629
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 202
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Schizosaccharomyces pombe
 ; FEATURE:
 ; OTHER INFORMATION: Karyophilic peptide
 US-09-876-904A-202

Query Match 27.3%; Score 3; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KSK 10
 |||
 Db 4 KSK 6

RESULT 18

US-09-876-904A-236

; Sequence 236, Application US/09876904A
 ; Publication No. US20030072794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOULIKAS, TENI
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
 THERAPEUTIC
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
 PEPTIDE
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
 ; FILE REFERENCE: TB-2002.00
 ; CURRENT APPLICATION NUMBER: US/09/876,904A
 ; CURRENT FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: US 60/210,925
 ; PRIOR FILING DATE: 2000-06-09
 ; NUMBER OF SEQ ID NOS: 629
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 236
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Unknown Organism
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: Hydrophilic protein
 US-09-876-904A-236

Query Match 27.3%; Score 3; DB 10; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 7 ARK 9

RESULT 19

US-09-876-904A-237

; Sequence 237, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 237
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Hydrophilic protein
US-09-876-904A-237

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ERK 8
|||
Db 1 ERK 3

RESULT 20

US-09-876-904A-509

; Sequence 509, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 509
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Ig/EBP-1 (immunoglobulin
; OTHER INFORMATION: gene enhancer-binding protein).
US-09-876-904A-509

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KSK 10
|||
Db 7 KSK 9

RESULT 21

US-09-876-904A-555

; Sequence 555, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 555
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human UsnRNP-associated 70 k protein (437 aas)
; OTHER INFORMATION: that is phosphorylated at Arg/Ser-rich domains.
US-09-876-904A-555

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ERK 8
|||
Db 5 ERK 7

RESULT 22

US-09-992-665-55

; Sequence 55, Application US/09992665
 ; Publication No. US20030092009A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaia Palm
 ; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
 ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
 ; FILE REFERENCE: CEMINES.002A
 ; CURRENT APPLICATION NUMBER: US/09/992,665
 ; CURRENT FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: 60/249,508
 ; PRIOR FILING DATE: 2000-11-16
 ; NUMBER OF SEQ ID NOS: 380
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 55
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Probe

US-09-992-665-55

Query Match 27.3%; Score 3; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SKD 11
 |||
 Db 2 SKD 4

RESULT 23

US-09-972-656-6

; Sequence 6, Application US/09972656
 ; Publication No. US20030099647A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Deshpande, Rajendra
 ; APPLICANT: Tsai, Mei-Mei
 ; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-
 Gamma
 ; TITLE OF INVENTION: Neutralizing Activity
 ; FILE REFERENCE: A-799
 ; CURRENT APPLICATION NUMBER: US/09/972,656
 ; CURRENT FILING DATE: 2001-10-05
 ; NUMBER OF SEQ ID NOS: 135
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-972-656-6

Query Match 27.3%; Score 3; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 6 ARK 8

RESULT 24

US-09-829-922-4

; Sequence 4, Application US/09829922
; Publication No. US20030171537A1
; GENERAL INFORMATION:
; APPLICANT: Halazonetis, Thanos
; APPLICANT: Hartwig, Wolfgang
; TITLE OF INVENTION: Peptides and peptidomimetics with
; TITLE OF INVENTION: structural similarity to human p53 that activate p53
; TITLE OF INVENTION: function
; FILE REFERENCE: 2973.19998
; CURRENT APPLICATION NUMBER: US/09/829,922
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 08/894,327
; PRIOR FILING DATE: 1997-12-04
; PRIOR APPLICATION NUMBER: pctus96/01535
; PRIOR FILING DATE: 1996-02-16
; PRIOR APPLICATION NUMBER: 08/392,542
; PRIOR FILING DATE: 1995-02-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-922-4

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KSK 10
|||
Db 8 KSK 10

RESULT 25

US-09-829-922-13

; Sequence 13, Application US/09829922
; Publication No. US20030171537A1
; GENERAL INFORMATION:
; APPLICANT: Halazonetis, Thanos
; APPLICANT: Hartwig, Wolfgang
; TITLE OF INVENTION: Peptides and peptidomimetics with
; TITLE OF INVENTION: structural similarity to human p53 that activate p53
; TITLE OF INVENTION: function
; FILE REFERENCE: 2973.19998
; CURRENT APPLICATION NUMBER: US/09/829,922
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 08/894,327
; PRIOR FILING DATE: 1997-12-04

; PRIOR APPLICATION NUMBER: pctus96/01535
; PRIOR FILING DATE: 1996-02-16
; PRIOR APPLICATION NUMBER: 08/392,542
; PRIOR FILING DATE: 1995-02-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic, modified from Homo sapiens p53
US-09-829-922-13

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KSK 10
|||
Db 2 KSK 4

RESULT 26

US-09-940-316B-57
; Sequence 57, Application US/09940316B
; Publication No. US20030175901A1
; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTI, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDES ENCODING THE fkbA GENE OF THE FK-520
POLYKETIDE SYNTHASE
; TITLE OF INVENTION: GENE CLUSTER
; FILE REFERENCE: 30062-20026.11
; CURRENT APPLICATION NUMBER: US/09/940,316B
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/410,551
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
; OTHER INFORMATION: synthase fragment

US-09-940-316B-57

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RER 7
|||
Db 5 RER 7

RESULT 27

US-10-430-685-39

; Sequence 39, Application US/10430685
; Publication No. US20040039543A1
; GENERAL INFORMATION:
; APPLICANT: KECK, Peter
; TITLE OF INVENTION: COMPUTER METHOD AND APPARATUS FOR CLASSIFYING OBJECTS
; FILE REFERENCE: 63040-010210
; CURRENT APPLICATION NUMBER: US/10/430,685
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/US01/44000
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/246,196
; PRIOR FILING DATE: 2000-11-06
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-430-685-39

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKS 9
|||
Db 3 RKS 5

RESULT 28

US-10-462-452-276

; Sequence 276, Application US/10462452
; Publication No. US20040037809A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd
; APPLICANT: Gupta, Malini
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
; FILE REFERENCE: 02-02US
; CURRENT APPLICATION NUMBER: US/10/462,452
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/393,066

; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 276
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-452-276

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TRE 6
|||
Db 1 TRE 3

RESULT 29

US-10-462-452-292

; Sequence 292, Application US/10462452
; Publication No. US20040037809A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd
; APPLICANT: Gupta, Malini
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
; FILE REFERENCE: 02-02US
; CURRENT APPLICATION NUMBER: US/10/462,452
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 292
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-452-292

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TRE 6
|||
Db 1 TRE 3

RESULT 30

US-10-462-452-308

; Sequence 308, Application US/10462452
; Publication No. US20040037809A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven

```
; APPLICANT: El Shafy, Mohammed Abd
; APPLICANT: Gupta, Malini
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
; FILE REFERENCE: 02-02US
; CURRENT APPLICATION NUMBER: US/10/462,452
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 308
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-452-308
```

```
Query Match          27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      4 TRE 6
      |||
Db      1 TRE 3
```

RESULT 31

```
US-10-462-452-324
; Sequence 324, Application US/10462452
; Publication No. US20040037809A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd
; APPLICANT: Gupta, Malini
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
; FILE REFERENCE: 02-02US
; CURRENT APPLICATION NUMBER: US/10/462,452
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 324
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-452-324
```

```
Query Match          27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      4 TRE 6
      |||
```

Db 1 TRE 3

RESULT 32

US-10-462-452-340

; Sequence 340, Application US/10462452
; Publication No. US20040037809A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd
; APPLICANT: Gupta, Malini
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
; FILE REFERENCE: 02-02US
; CURRENT APPLICATION NUMBER: US/10/462,452
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 340
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-452-340

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TRE 6
|||
Db 1 TRE 3

RESULT 33

US-10-462-452-356

; Sequence 356, Application US/10462452
; Publication No. US20040037809A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd
; APPLICANT: Gupta, Malini
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
; FILE REFERENCE: 02-02US
; CURRENT APPLICATION NUMBER: US/10/462,452
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 356
; LENGTH: 11
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-462-452-356

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TRE 6
|||
Db 1 TRE 3

RESULT 34

US-10-462-452-372

; Sequence 372, Application US/10462452
; Publication No. US20040037809A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd
; APPLICANT: Gupta, Malini
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
; FILE REFERENCE: 02-02US
; CURRENT APPLICATION NUMBER: US/10/462,452
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-452-372

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TRE 6
|||
Db 1 TRE 3

RESULT 35

US-10-462-452-388

; Sequence 388, Application US/10462452
; Publication No. US20040037809A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd
; APPLICANT: Gupta, Malini
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
; FILE REFERENCE: 02-02US

; CURRENT APPLICATION NUMBER: US/10/462,452
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 388
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-452-388

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TRE 6
|||
Db 1 TRE 3

RESULT 36

US-10-398-104-203
; Sequence 203, Application US/10398104
; Publication No. US20040047880A1
; GENERAL INFORMATION:
; APPLICANT: De Bolle, Xavier Thomas
; APPLICANT: Letesson, Jean-Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Mertens, Pascal Yvon
; APPLICANT: Poolman, Jan
; APPLICANT: Voet, Pierre
; TITLE OF INVENTION: COMPONENT FOR VACCINE
; FILE REFERENCE: B45242
; CURRENT APPLICATION NUMBER: US/10/398,104
; CURRENT FILING DATE: 2003-01-04
; PRIOR APPLICATION NUMBER: PCT/EP01/11409
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: GB 0024200.8
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 203
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LOS peptide mimotope sequence
US-10-398-104-203

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKT 4
|||
Db 7 RKT 9

RESULT 37

US-10-344-878-5

```
; Sequence 5, Application US/10344878
; Publication No. US20040053848A1
; GENERAL INFORMATION:
; APPLICANT: The University of Virginia Patent Foundation
; APPLICANT: Allis, C. David
; APPLICANT: Strahl, Brian D
; TITLE OF INVENTION: Antibodies Specific for Methylated Lysines in Histones
; FILE REFERENCE: 00601-02
; CURRENT APPLICATION NUMBER: US/10/344,878
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: US 60/227,767
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/302,747
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: synthetic peptide used to raise antibodies against the H3
amino t
;   OTHER INFORMATION: erminus having MeLys at the fifth amino acid position.
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (5)..(5)
;   OTHER INFORMATION: METHYLATION
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (10)..(11)
;   OTHER INFORMATION: artificial amino acids added to the natural histone
sequence to a
;   OTHER INFORMATION: id in the production of the antibody
US-10-344-878-5
```

```
Query Match          27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 ARK 3
        |||
Db      3 ARK 5
```

RESULT 38

US-10-344-878-6

```
; Sequence 6, Application US/10344878
; Publication No. US20040053848A1
; GENERAL INFORMATION:
; APPLICANT: The University of Virginia Patent Foundation
; APPLICANT: Allis, C. David
; APPLICANT: Strahl, Brian D
```

```

; TITLE OF INVENTION: Antibodies Specific for Methylated Lysines in Histones
; FILE REFERENCE: 00601-02
; CURRENT APPLICATION NUMBER: US/10/344,878
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: US 60/227,767
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/302,747
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide used to raise antibodies against the H3
amino t
; OTHER INFORMATION: erminus having MeLys at the fifth amino acid position.
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: METHYLATION
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (10)..(11)
; OTHER INFORMATION: artificial amino acids added to the natural histone
sequence to a
; OTHER INFORMATION: id in the production of the antibody
US-10-344-878-6

```

```

Query Match          27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 ARK 3
      |||
Db      3 ARK 5

```

```

RESULT 39
US-09-822-965-16
; Sequence 16, Application US/09822965
; Publication No. US20010029027A1
; GENERAL INFORMATION:
; APPLICANT: Innerarity, Thomas
; APPLICANT: Boren, Jan
; TITLE OF INVENTION: METHODS AND TOOLS FOR IDENTIFYING
; TITLE OF INVENTION: COMPOUNDS WHICH MODULATE ATHEROSCLEROSIS BY IMPACTING
; TITLE OF INVENTION: LDL-PROTEOGLYCAN BINDING
; FILE REFERENCE: 220002059710
; CURRENT APPLICATION NUMBER: US/09/822,965
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 09/265,222
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: US 60/077,618
; PRIOR FILING DATE: 1998-03-10
; NUMBER OF SEQ ID NOS: 25

```

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: 6
; OTHER INFORMATION: Insertion of a single amino acid
US-09-822-965-16

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TRE 6
|||
Db 4 TRE 6

RESULT 40
US-09-823-418-16
; Sequence 16, Application US/09823418
; Publication No. US20010024797A1
; GENERAL INFORMATION:
; APPLICANT: Innerarity, Thomas
; APPLICANT: Boren, Jan
; TITLE OF INVENTION: METHODS AND TOOLS FOR IDENTIFYING COMPOUNDS
; TITLE OF INVENTION: WHICH MODULATE ATHEROSCLEROSIS BY IMPACTING
; TITLE OF INVENTION: LDL-PROTEOGLYCAN BINDING
; FILE REFERENCE: 220002059711
; CURRENT APPLICATION NUMBER: US/09/823,418
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 09/265,222
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: US 60/077,618
; PRIOR FILING DATE: 1998-03-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: 6
; OTHER INFORMATION: Insertion of a single amino acid
US-09-823-418-16

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TRE 6
|||
Db 4 TRE 6

RESULT 41

US-10-044-034-14

```
; Sequence 14, Application US/10044034
; Publication No. US20020169264A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, DAVID C.
; APPLICANT: O'BRIEN-SIMPSON, NEIL M.
; APPLICANT: BROWN, LORENA E.
; APPLICANT: EDE, NICHOLAS J.
; APPLICANT: BRANDT, EVELYN R.
; APPLICANT: GOOD, MICHAEL F.
; TITLE OF INVENTION: POLYMERS INCORPORATING PEPTIDES
; FILE REFERENCE: FBRC:006
; CURRENT APPLICATION NUMBER: US/10/044,034
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: P05071
; PRIOR FILING DATE: 1997-02-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptides
```

US-10-044-034-14

```
Query Match          27.3%; Score 3; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      6 ERK 8
      |||
Db      7 ERK 9
```

RESULT 42

US-10-124-880-30

```
; Sequence 30, Application US/10124880
; Publication No. US20030026810A1
; GENERAL INFORMATION:
; APPLICANT: Jorgensen, Per Lina
; APPLICANT: Schnorr, Kirk
; APPLICANT: Andersen, Lene No. US20030026810Alboe
; APPLICANT: Schulein, Martin
; APPLICANT: Outtrup, Helle
; TITLE OF INVENTION: No. US20030026810A1el Rhamnogalacturonan Hydrolases
; FILE REFERENCE: 5572.204-US
; CURRENT APPLICATION NUMBER: US/10/124,880
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US/09/311,626B
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 0608/98
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: 60/084,358
```

; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Microbial
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6
; OTHER INFORMATION: Xaa= Ser or Thr
US-10-124-880-30

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SKD 11
|||
Db 8 SKD 10

RESULT 43

US-10-062-710-165

; Sequence 165, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV B Cell Epitopes
US-10-062-710-165

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RER 7
|||
Db 8 RER 10

RESULT 44

US-10-062-710-166

; Sequence 166, Application US/10062710
 ; Publication No. US20030049253A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Frank Q.
 ; APPLICANT: Chu, Yong-Liang
 ; APPLICANT: Qiu, Jian-Tai
 ; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
 ; TITLE OF INVENTION: MHC-Recognized Epitopes
 ; TITLE OF INVENTION: Via Peptide Vaccines
 ; FILE REFERENCE: 3781-001-27
 ; CURRENT APPLICATION NUMBER: US/10/062,710
 ; CURRENT FILING DATE: 2002-02-05
 ; PRIOR APPLICATION NUMBER: US 60/310,498
 ; PRIOR FILING DATE: 2001-08-08
 ; NUMBER OF SEQ ID NOS: 232
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 166
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: HIV B Cell Epitopes
 US-10-062-710-166

Query Match 27.3%; Score 3; DB 14; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RER 7
 |||
 Db 4 RER 6

RESULT 45

US-10-044-995-3

; Sequence 3, Application US/10044995
 ; Publication No. US20030049685A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DELEYS, ROBERT J
 ; POLLET, DIRK
 ; MAERTENS, GEERT
 ; VAN HEUVERSWUN, HUGO
 ; TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF
 ; ANTIBODIES TO HEPATITIS C VIRUS
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE P.C.
 ; STREET: 1100 NORTH GLEBE ROAD
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22201
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

```

;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/10/044,995
;       FILING DATE: 15-Jan-2002
;       CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/391,671
;       FILING DATE: <Unknown>
;       APPLICATION NUMBER: US 07/920,286
;       FILING DATE: 14-OCT-1992
;       APPLICATION NUMBER: WO PCT/EP91/02409
;       FILING DATE: 13-DEC-1991
;       APPLICATION NUMBER: EP 90124241.2
;       FILING DATE: 14-DEC-1990
;       ATTORNEY/AGENT INFORMATION:
;       NAME: SADOFF, B.J.
;       REGISTRATION NUMBER: 36,663
;       REFERENCE/DOCKET NUMBER: 1487-5
;       TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 7038164000
;       TELEFAX: 7038164100
;       INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;       LENGTH: 11 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-044-995-3

```

```

Query Match          27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 RKT 4
      |||
Db      2 RKT 4

```

```

RESULT 46
US-10-229-915-21
; Sequence 21, Application US/10229915
; Publication No. US20030083262A1
; GENERAL INFORMATION:
; APPLICANT: Lazarus, Douglas
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING INFLAMMATORY
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: PPI-127
; CURRENT APPLICATION NUMBER: US/10/229,915
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/316,328
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0

```

; SEQ ID NO 21
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: anti-inflammatory compound
US-10-229-915-21

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
|||
Db 2 ARK 4

RESULT 47

US-10-211-088-202
; Sequence 202, Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For
Molecular Binding
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Nuclear localization signal
US-10-211-088-202

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKS 9
|||
Db 4 RKS 6

RESULT 48

US-10-136-738-2
; Sequence 2, Application US/10136738
; Publication No. US20030108886A1


```
; GENERAL INFORMATION:
; APPLICANT: Finn, John
; APPLICANT: MacLachlan, Ian
; APPLICANT: Protiva Biotherapeutics Inc.
; TITLE OF INVENTION: Autogene Nucleic Acids Encoding a
; TITLE OF INVENTION: Secretable RNA Polymerase
; FILE REFERENCE: 020801-000310US
; CURRENT APPLICATION NUMBER: US/10/136,738
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/287,974
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-Tat variant secretion domain
US-10-136-738-2
```

```
Query Match          27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      1 ARK 3
        |||
Db      2 ARK 4
```

```
RESULT 49
US-10-213-512-212
; Sequence 212, Application US/10213512
; Publication No. US20030110536A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; FILE REFERENCE: 023070-086110US
; CURRENT APPLICATION NUMBER: US/10/213,512
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: US/09/177,206
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: US 09/071,838
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 11
; TYPE: PRT
```

; ORGANISM: Arabidopsis sp.
US-10-213-512-212

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RKS 9
|||
Db 2 RKS 4

RESULT 50

US-10-213-512-253

; Sequence 253, Application US/10213512
; Publication No. US20030110536A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; FILE REFERENCE: 023070-086110US
; CURRENT APPLICATION NUMBER: US/10/213,512
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: US/09/177,206
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: US 09/071,838
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 253
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-10-213-512-253

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ERK 8
|||
Db 5 ERK 7

RESULT 51

US-10-197-954-48

; Sequence 48, Application US/10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
; APPLICANT: K"ster, Hubert

```

; APPLICANT: Siddiqi, Suhaib
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US/10/197,954
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Homo Sapien
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: 11
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: 1
;   OTHER INFORMATION: Xaa is pyroglutamic acid
US-10-197-954-48

```

```

Query Match          27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 SKD 11
      |||
Db      3 SKD 5

```

RESULT 52

US-10-160-290-4

```

; Sequence 4, Application US/10160290
; Publication No. US20030124557A1
;   GENERAL INFORMATION:
;       APPLICANT: Halazonetis, Thanos
;               Hartwig, Wolfgang
;       TITLE OF INVENTION: Peptides nad Peptidomimetics with
;               Structural Similarity to Human p53 That Activate
;               p53
;               Function
;       NUMBER OF SEQUENCES: 35
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Banner, Birch, McKie & Beckett
;           STREET: 1001 G Street, N.W.
;           CITY: Washington, D.C.
;           STATE: District of Columbia
;           COUNTRY: U.S.
;           ZIP: 20001

```

```

;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/10/160,290
;      FILING DATE: 04-Jun-2002
;      CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US/09/685,027
;      FILING DATE: 10-Oct-2000
;      APPLICATION NUMBER: 08/392,542
;      FILING DATE: <Unknown>
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Posorske, Laurence H.
;      REGISTRATION NUMBER: 34,698
;      REFERENCE/DOCKET NUMBER: 0486.48439
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 202 508-9100
;      TELEFAX: 202 508-9299
;      INFORMATION FOR SEQ ID NO: 4:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 11 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: peptide
;      SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-160-290-4

```

```

Query Match          27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 KSK 10
      |||
Db      8 KSK 10

```

```

RESULT 53
US-10-160-290-13
; Sequence 13, Application US/10160290
; Publication No. US20030124557A1
; GENERAL INFORMATION:
; APPLICANT: Halazonetis, Thanos
;           Hartwig, Wolfgang
; TITLE OF INVENTION: Peptides nad Peptidomimetics with
;                   Structural Similarity to Human p53 That Activate
;                   p53
;                   Function
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.

```

```

;      ZIP: 20001
;
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25
;
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/10/160,290
;      FILING DATE: 04-Jun-2002
;      CLASSIFICATION: <Unknown>
;
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US/09/685,027
;      FILING DATE: 10-Oct-2000
;      APPLICATION NUMBER: 08/392,542
;      FILING DATE: <Unknown>
;
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Posorske, Laurence H.
;      REGISTRATION NUMBER: 34,698
;      REFERENCE/DOCKET NUMBER: 0486.48439
;
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 202 508-9100
;      TELEFAX: 202 508-9299
;
;      INFORMATION FOR SEQ ID NO: 13:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 11 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;
;      MOLECULE TYPE: peptide
;
;      SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-160-290-13

```

```

Query Match          27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 KSK 10
      |||
Db      2 KSK 4

```

RESULT 54

US-10-234-579-12

; Sequence 12, Application US/10234579

; Publication No. US20030129587A1

; GENERAL INFORMATION:

```

;      APPLICANT: SALLBERG, MATTI
;      TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
;                          EXCHANGER
;
;      NUMBER OF SEQUENCES: 23
;      CORRESPONDENCE ADDRESS:
;      ADDRESSEE: DARBY & DARBY PC
;      STREET: 805 Third Avenue
;      CITY: New York
;      STATE: New York
;      COUNTRY: USA
;      ZIP: 10022
;
;      COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/234,579
; FILING DATE: 30-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,085
; FILING DATE: 27-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 3846/OC569
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7659
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-234-579-12

```

```

Query Match          27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 RKT 4
      |||
Db      2 RKT 4

```

```

RESULT 55
US-10-195-730-318
; Sequence 318, Application US/10195730
; Publication No. US20030144492A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et. al
; TITLE OF INVENTION: 101 Human Secreted Proteins
; FILE REFERENCE: PZ017P1
; CURRENT APPLICATION NUMBER: US/10/195,730
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: US/09/281,976
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/060,837
; PRIOR FILING DATE: 1997-10-02
; PRIOR APPLICATION NUMBER: 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 390
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 318

```

; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-730-318

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ERK 8
|||
Db 8 ERK 10

RESULT 56

US-10-032-201B-310

; Sequence 310, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijs
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND
RELATED
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-032-201B-310

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SKD 11
|||
Db 4 SKD 6

RESULT 57

US-10-224-999A-2198

; Sequence 2198, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott

```
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2198
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Rubella virus
US-10-224-999A-2198
```

```
Query Match          27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      5 RER 7
      |||
Db      5 RER 7
```

RESULT 58

```
US-10-224-999A-2199
; Sequence 2199, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2199
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Rubella virus
US-10-224-999A-2199
```

```
Query Match          27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      5 RER 7
      |||
Db      4 RER 6
```


RESULT 59

US-10-224-999A-2200

; Sequence 2200, Application US/10224999A
 ; Publication No. US20030171318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Inc.
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Zavitz, Kenton
 ; APPLICANT: Hobden, Adrian
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
 ; FILE REFERENCE: 5004.01
 ; CURRENT APPLICATION NUMBER: US/10/224,999A
 ; CURRENT FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/313,695
 ; PRIOR FILING DATE: 2001-08-20
 ; NUMBER OF SEQ ID NOS: 3484
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2200
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Rubella virus
 US-10-224-999A-2200

Query Match 27.3%; Score 3; DB 14; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RER 7
 |||
 Db 3 RER 5

RESULT 60

US-10-224-999A-2201

; Sequence 2201, Application US/10224999A
 ; Publication No. US20030171318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Inc.
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Zavitz, Kenton
 ; APPLICANT: Hobden, Adrian
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
 ; FILE REFERENCE: 5004.01
 ; CURRENT APPLICATION NUMBER: US/10/224,999A
 ; CURRENT FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/313,695
 ; PRIOR FILING DATE: 2001-08-20
 ; NUMBER OF SEQ ID NOS: 3484
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2201
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Rubella virus
 US-10-224-999A-2201

Query Match 27.3%; Score 3; DB 14; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RER 7
|||
Db 2 RER 4

RESULT 61

US-10-224-999A-2202

; Sequence 2202, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2202
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Rubella virus
US-10-224-999A-2202

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RER 7
|||
Db 1 RER 3

RESULT 62

US-10-168-445-83

; Sequence 83, Application US/10168445
; Publication No. US20030177518A1
; GENERAL INFORMATION:
; APPLICANT: Osbourn, Anne E
; APPLICANT: Haralampidis, Kosmas
; APPLICANT: Bryan, Gregory T
; TITLE OF INVENTION: Plant Gene
; FILE REFERENCE: 0380-P02892US0
; CURRENT APPLICATION NUMBER: US/10/168,445
; CURRENT FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: PCT/GB00/04908
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: GB 9930394.3
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: GB 0020217.6
; PRIOR FILING DATE: 2000-08-16

; NUMBER OF SEQ ID NOS: 219
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 83
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Avena strigosa
US-10-168-445-83

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKS 9
|||
Db 7 RKS 9

RESULT 63

US-10-105-232-108

; Sequence 108, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 108
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Influenza B virus
US-10-105-232-108

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KSK 10
|||
Db 9 KSK 11

RESULT 64

US-10-161-791-283

; Sequence 283, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 283:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-283

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KTR 5
|||
Db 9 KTR 11

RESULT 65

US-10-405-339-13

; Sequence 13, Application US/10405339
 ; Publication No. US20030190364A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Panitch, Alyssa
 ; APPLICANT: Seal, Brandon
 ; TITLE OF INVENTION: Biological Affinity Based Delivery Systems
 ; FILE REFERENCE: 9138-0079US
 ; CURRENT APPLICATION NUMBER: US/10/405,339
 ; CURRENT FILING DATE: 2003-04-01
 ; PRIOR APPLICATION NUMBER: US 60/369,568
 ; PRIOR FILING DATE: 2002-04-01
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 13
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic peptide
 US-10-405-339-13

Query Match 27.3%; Score 3; DB 14; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3
 |||
 Db 2 ARK 4

RESULT 66

US-10-189-437-95

; Sequence 95, Application US/10189437
 ; Publication No. US20030194414A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOGOCH, SAMUEL
 ; APPLICANT: BOGOCH, ELENORE S.
 ; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
 ; FILE REFERENCE: 09425/46905
 ; CURRENT APPLICATION NUMBER: US/10/189,437
 ; CURRENT FILING DATE: 2002-07-08
 ; PRIOR APPLICATION NUMBER: 10/105,232
 ; PRIOR FILING DATE: 2002-03-26
 ; PRIOR APPLICATION NUMBER: 09/984,057
 ; PRIOR FILING DATE: 2001-10-26
 ; PRIOR APPLICATION NUMBER: 60/303,396
 ; PRIOR FILING DATE: 2001-07-09
 ; PRIOR APPLICATION NUMBER: 60/278,761
 ; PRIOR FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 729
 ; SOFTWARE: PatentIn 2.1
 ; SEQ ID NO 95
 ; LENGTH: 11
 ; TYPE: PRT

; ORGANISM: Influenza B virus
US-10-189-437-95

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KSK 10
|||
Db 9 KSK 11

RESULT 67

US-10-411-869A-30
; Sequence 30, Application US/10411869A
; Publication No. US20030228605A1
; GENERAL INFORMATION:
; APPLICANT: Slootstra, Jelle Wouter
; APPLICANT: Puijk, Wouter Cornelis
; APPLICANT: Meloen, Robert Hans
; APPLICANT: van Dijk, Evert
; APPLICANT: van Dijken, Pieter
; TITLE OF INVENTION: IDENTIFICATION OF PROTEIN BINDING SITES
; FILE REFERENCE: 2183-5921US (SVD/P54407US00)
; CURRENT APPLICATION NUMBER: US/10/411,869A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/NL01/00744
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: EP 00203518.6
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: HCDR3 of 1fld.pdb
US-10-411-869A-30

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RER 7
|||
Db 2 RER 4

RESULT 68

US-10-378-173-136
; Sequence 136, Application US/10378173
; Publication No. US20030232014A1
; GENERAL INFORMATION:
; APPLICANT: Burke et al.
; TITLE OF INVENTION: PHOSPHORYLATED PROTEINS AND USES RELATED THERETO
; FILE REFERENCE: MDSP-P01-023

```

; CURRENT APPLICATION NUMBER: US/10/378,173
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 60/360787
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 136
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: phosphorylated peptide
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (3)..(3)
; OTHER INFORMATION: phosphorylation
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (4)..(4)
; OTHER INFORMATION: phosphorylation
US-10-378-173-136

```

```

Query Match          27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      7 RKS 9
      |||
Db      1 RKS 3

```

RESULT 69

US-10-014-099F-30

```

; Sequence 30, Application US/10014099F
; Publication No. US20040003420A1
; GENERAL INFORMATION:
; APPLICANT: KUEHN, Ralf
; APPLICANT: FELDER, Susanne
; APPLICANT: SCHWENK, Frieder
; APPLICANT: KUETER-LUKS, Birgit
; APPLICANT: FAUST, Nicole
; TITLE OF INVENTION: Modified Recombinase
; FILE REFERENCE: 012787wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/014,099F
; CURRENT FILING DATE: 2001-11-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NLS
US-10-014-099F-30

```

```

Query Match          27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;

```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RKS 9
|||
Db 4 RKS 6

RESULT 70

US-10-443-622-90

; Sequence 90, Application US/10443622
; Publication No. US20040024192A1
; GENERAL INFORMATION:
; APPLICANT: Carter et al.
; TITLE OF INVENTION: 19 Human Secreted Proteins
; FILE REFERENCE: PZ009P1
; CURRENT APPLICATION NUMBER: US/10/443,622
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US98/13608
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: 60/051,480
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 60/051,381
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 60/058,663
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,598
; PRIOR FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-443-622-90

Query Match 27.3%; Score 3; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TRE 6
|||
Db 3 TRE 5

RESULT 71

US-08-996-470-2

; Sequence 2, Application US/08996470A
; Publication No. US20020077314A1
; GENERAL INFORMATION:
; APPLICANT: Falk
; TITLE OF INVENTION: Use of Hyaluronic Acid and Forms to Prevent Arterial
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/996,470A
; CURRENT FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: US 07/675,908
; EARLIER FILING DATE: 1991-07-03


```

; EARLIER APPLICATION NUMBER: US 07/838,674
; EARLIER FILING DATE: 1992-02-21
; EARLIER APPLICATION NUMBER: US 07/838,675
; EARLIER FILING DATE: 1992-02-21
; EARLIER APPLICATION NUMBER: US 08/125,398
; EARLIER FILING DATE: 1993-09-23
; EARLIER APPLICATION NUMBER: US 08/285,764
; EARLIER FILING DATE: 1994-08-03
; EARLIER APPLICATION NUMBER: US 07/952,095
; EARLIER FILING DATE: 1992-09-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)..(11)
; OTHER INFORMATION: Scrambled peptide consisting of randomly arranged
; OTHER INFORMATION: amino acids 401-411 located in the hyaluronic acid
; OTHER INFORMATION: binding region of RHAMM
US-08-996-470-2

```

```

Query Match          18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.5e+04;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 KS 9
      ||
Db      10 KS 11

```

RESULT 72

US-08-424-550B-223

; Sequence 223, Application US/08424550B

; Publication No. US20020119447A1

; GENERAL INFORMATION:

; APPLICANT: JOHN N. SIMONS

; APPLICANT: TAMI J. PILOT-MATIAS

; APPLICANT: GEORGE J. DAWSON

; APPLICANT: GEORGE G. SCHLAUDER

; APPLICANT: SURESH M. DESAI

; APPLICANT: THOMAS P. LEARY

; APPLICANT: ANTHONY SCOTT MUERHOFF

; APPLICANT: JAMES C. ERKER

; APPLICANT: SHERI L. BUIJK

; APPLICANT: ISA K. MUSHAHWAR

; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS

; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE

; NUMBER OF SEQUENCES: 716

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D

; STREET: 100 ABBOTT PARK ROAD

; CITY: ABBOTT PARK

; STATE: IL

; COUNTRY: USA

```

; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 223:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-223

```

```

Query Match          18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.5e+04;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      4 TR 5
      ||
Db      10 TR 11

```

RESULT 73

US-08-424-550B-523

```

; Sequence 523, Application US/08424550B
; Publication No. US20020119447A1

```

GENERAL INFORMATION:

```

; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAHWAR
; TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL

```

```

; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 523:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-523

```

```

Query Match          18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.5e+04;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AR 2
      ||
Db      8 AR 9

```

RESULT 74

```

US-08-424-550B-550
; Sequence 550, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAHWAR
; TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK

```

```

; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 550:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-550

```

```

Query Match          18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.5e+04;
Matches      2; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      8 KS 9
      ||
Db      4 KS 5

```

RESULT 75

US-08-809-423A-5

```

; Sequence 5, Application US/08809423A
; Publication No. US20020169104A1
; GENERAL INFORMATION:
; APPLICANT: FRANK, GLENN R.
; APPLICANT: HUNTER, SHIRLEY WU
; APPLICANT: WALLENFELS, LYNDIA
; TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
; TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,423A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CONNELL, GARY J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-17-C2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-423A-5

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KT 4
||
Db 6 KT 7

Search completed: April 8, 2004, 16:35:46
Job time : 31.3077 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 27.7692 Seconds
(without alignments)
124.984 Million cell updates/sec

Title: US-09-787-443A-14
Perfect score: 11
Sequence: 1 ARKTRERKSKD 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 460

Minimum DB seq length: 11
Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8
Result Query
No. Score Match Length DB ID Description

1	3	27.3	11	4	O94785	O94785 homo sapien
2	3	27.3	11	4	Q9H3V7	Q9h3v7 homo sapien
3	3	27.3	11	10	Q9S8X4	Q9s8x4 glycine max
4	3	27.3	11	11	Q9JLE6	Q9jle6 rattus norv
5	2	18.2	11	2	Q8RKN1	Q8rkn1 escherichia
6	2	18.2	11	2	P77404	P77404 escherichia
7	2	18.2	11	2	Q8RMI8	Q8rmi8 enterococcu
8	2	18.2	11	2	Q9K332	Q9k332 staphylococ
9	2	18.2	11	2	Q47345	Q47345 escherichia
10	2	18.2	11	2	Q9R872	Q9r872 escherichia
11	2	18.2	11	2	Q91UY9	Q9luy9 escherichia
12	2	18.2	11	3	Q9C1R7	Q9clr7 saccharomyc
13	2	18.2	11	4	Q14759	Q14759 homo sapien
14	2	18.2	11	4	Q9Y3G2	Q9y3g2 homo sapien
15	2	18.2	11	4	Q16427	Q16427 homo sapien
16	2	18.2	11	4	Q9UCP5	Q9ucp5 homo sapien
17	2	18.2	11	4	Q9UC46	Q9uc46 homo sapien
18	2	18.2	11	5	Q25916	Q25916 plasmodium
19	2	18.2	11	5	Q9NFX0	Q9nfx0 drosophila
20	2	18.2	11	5	Q8MM58	Q8mm58 heliconius
21	2	18.2	11	5	Q95PX6	Q95px6 caenorhabdi
22	2	18.2	11	6	Q9TRW5	Q9trw5 bos taurus
23	2	18.2	11	6	Q9TQS0	Q9tqs0 bos taurus
24	2	18.2	11	7	O78119	O78119 oreochromis
25	2	18.2	11	7	O77911	O77911 oreochromis
26	2	18.2	11	7	O77908	O77908 oreochromis
27	2	18.2	11	7	O77893	O77893 oreochromis
28	2	18.2	11	8	Q94V94	Q94v94 varanus sto
29	2	18.2	11	8	Q9G646	Q9g646 sitana pont
30	2	18.2	11	8	Q9G5W2	Q9g5w2 laudakia tu
31	2	18.2	11	8	Q9G631	Q9g631 calotes nig
32	2	18.2	11	8	Q9G622	Q9g622 salea horsf
33	2	18.2	11	8	Q94VG8	Q94vg8 varanus gou
34	2	18.2	11	8	Q9G365	Q9g365 calotes emm
35	2	18.2	11	8	Q9G5Y6	Q9g5y6 agama agama
36	2	18.2	11	8	Q8MEL7	Q8mel7 sida hooker
37	2	18.2	11	8	Q9G5Y0	Q9g5y0 pseudotrape
38	2	18.2	11	8	Q9G5W5	Q9g5w5 laudakia nu
39	2	18.2	11	8	Q9G607	Q9g607 aphaniotis
40	2	18.2	11	8	Q94V77	Q94v77 heloderma s
41	2	18.2	11	8	Q9G628	Q9g628 calotes mys
42	2	18.2	11	8	O79985	O79985 laudakia ca
43	2	18.2	11	8	Q94VI5	Q94vi5 varanus exa
44	2	18.2	11	8	Q9G359	Q9g359 japalura fl
45	2	18.2	11	8	Q8MEM2	Q8mem2 lagunaria p
46	2	18.2	11	8	Q9G649	Q9g649 otocryptis
47	2	18.2	11	8	Q9G643	Q9g643 calotes cal
48	2	18.2	11	8	Q9G5X4	Q9g5x4 trapelus ag
49	2	18.2	11	8	Q94V74	Q94v74 lanthanotus
50	2	18.2	11	8	Q8MES5	Q8mes5 abelmoschus
51	2	18.2	11	8	Q9G616	Q9g616 ceratophora
52	2	18.2	11	8	Q9G350	Q9g350 laudakia sa
53	2	18.2	11	8	Q9G610	Q9g610 lyriocephal
54	2	18.2	11	8	O79636	O79636 laudakia hi
55	2	18.2	11	8	Q9G5Z8	Q9g5z8 acanthosaur
56	2	18.2	11	8	Q9G5W8	Q9g5w8 trapelus sa
57	2	18.2	11	8	Q8MEP0	Q8mep0 hibiscus pe

58	2	18.2	11	8	Q8MER8	Q8mer8	dombeya	til
59	2	18.2	11	8	Q9G5V3	Q9g5v3	phrynocepha	
60	2	18.2	11	8	Q94VE7	Q94ve7	varanus	kom
61	2	18.2	11	8	Q8WES0	Q8wes0	ceratophora	
62	2	18.2	11	8	Q94VB8	Q94vb8	varanus	sal
63	2	18.2	11	8	Q9G634	Q9g634	calotes	lio
64	2	18.2	11	8	Q9G353	Q9g353	trapelus	sa
65	2	18.2	11	8	O79642	O79642	laudakia	mi
66	2	18.2	11	8	Q8MES1	Q8mes1	alyogyne	pi
67	2	18.2	11	8	Q94VH7	Q94vh7	varanus	gil
68	2	18.2	11	8	Q8SKR0	Q8skr0	rankinia	di
69	2	18.2	11	8	Q9G601	Q9g601	bronchocela	
70	2	18.2	11	8	Q8MEP3	Q8mep3	hibiscus	no
71	2	18.2	11	8	Q9G619	Q9g619	ceratophora	
72	2	18.2	11	8	Q8WER7	Q8wer7	ceratophora	
73	2	18.2	11	8	Q8WD50	Q8wd50	ceratophora	
74	2	18.2	11	8	Q94VK1	Q94vk1	varanus	aca
75	2	18.2	11	8	Q9G5X7	Q9g5x7	trapelus	ru
76	2	18.2	11	8	Q9G356	Q9g356	agama	atra
77	2	18.2	11	8	O79639	O79639	laudakia	le
78	2	18.2	11	8	Q8MEQ7	Q8meq7	hibiscus	dr
79	2	18.2	11	8	Q9G613	Q9g613	cophotis	ce
80	2	18.2	11	8	Q9G5V0	Q9g5v0	laudakia	st
81	2	18.2	11	8	Q8MEL9	Q8mel9	pavonia	has
82	2	18.2	11	8	Q9G5V6	Q9g5v6	phrynocepha	
83	2	18.2	11	8	Q9G5X1	Q9g5x1	trapelus	pe
84	2	18.2	11	8	Q9G625	Q9g625	calotes	ver
85	2	18.2	11	8	Q9G5Z5	Q9g5z5	japalura	sp
86	2	18.2	11	8	Q9G5Z2	Q9g5z2	pseudocalot	
87	2	18.2	11	8	Q9G640	Q9g640	calotes	cey
88	2	18.2	11	8	Q8MER0	Q8mer0	hibiscus	co
89	2	18.2	11	8	Q8MES3	Q8mes3	alyogyne	cr
90	2	18.2	11	8	Q8WER4	Q8wer4	ceratophora	
91	2	18.2	11	8	Q8MEP5	Q8mep5	hibiscus	mi
92	2	18.2	11	8	O79986	O79986	laudakia	er
93	2	18.2	11	8	Q8MER1	Q8mer1	hibiscus	ca
94	2	18.2	11	8	Q9G604	Q9g604	gonocephalu	
95	2	18.2	11	8	Q9G652	Q9g652	japalura	va
96	2	18.2	11	8	Q9G655	Q9g655	japalura	tr
97	2	18.2	11	8	Q9G637	Q9g637	calotes	lio
98	2	18.2	11	8	Q9G5V9	Q9g5v9	laudakia	st
99	2	18.2	11	8	Q9G5Y9	Q9g5y9	pseudocalot	
100	2	18.2	11	8	Q8MER7	Q8mer7	fioria	viti

ALIGNMENTS

RESULT 1

O94785

ID O94785 PRELIMINARY; PRT; 11 AA.
AC O94785;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Thrombopoietin (Fragment).
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki Y., Takahashi T., Nakamura K., Okuno Y., Nakao K.;
 RT "Production of Thrombopoietin by Human Carcinomas and Its Novel mRNA
 RT Isoforms.";
 RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB014683; BAA34932.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1203 MW; 5FE19F44B6C1A877 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TRE 6
 |||
 Db 8 TRE 10

RESULT 2

Q9H3V7

ID Q9H3V7 PRELIMINARY; PRT; 11 AA.
 AC Q9H3V7;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Aquaporin-4 (Fragment).
 GN AQP4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97008105; PubMed=8855281;
 RA Lu M., Lee M.D., Smith B.L., Jung J.S., Agre P., Verdijk M.A.J.,
 RA Merckx G., Rijss J.P.L., Deen P.M.T.;
 RT "The human AQP4 gene: definition of the locus encoding two water
 RT channel polypeptides in brain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:10908-10912(1996).
 DR EMBL; U63613; AAG17964.1; -.
 DR GO; GO:0005372; F:water transporter activity; NAS.
 DR GO; GO:0006833; P:water transport; NAS.
 KW Porin.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1233 MW; 379D9CA311AEB737 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TRE 6
 |||

RESULT 3

Q9S8X4

ID Q9S8X4 PRELIMINARY; PRT; 11 AA.
 AC Q9S8X4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Vegetative storage protein 94 peptide 3, VSP94=LIPOXYGENASE
 DE (Fragment).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92361246; PubMed=1822994;
 RA Tranbarger T.J., Franceschi V.R., Hildebrand D.F., Grimes H.D.;
 RT "The soybean 94-kilodalton vegetative storage protein is a
 RT lipoxygenase that is localized in paraveinal mesophyll cell
 RT vacuoles."
 RL Plant Cell 3:973-987(1991).
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1366 MW; 9B337C3C0DD9CB1A CRC64;

Query Match 27.3%; Score 3; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RER 7
 |||
 Db 8 RER 10

RESULT 4

Q9JLE6

ID Q9JLE6 PRELIMINARY; PRT; 11 AA.
 AC Q9JLE6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Thioredoxin reductase (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rundlof A.-K., Arner E.S.J.;
 RT "Genomic sequence of parts of the rat thioredoxin reductase 1 gene."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF189711; AAF26304.1; -.
 FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1255 MW; 804D1A1E6DDAA325 CRC64;

Query Match 27.3%; Score 3; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SKD 11
|||
Db 4 SKD 6

RESULT 5

Q8RKN1

ID Q8RKN1 PRELIMINARY; PRT; 11 AA.
AC Q8RKN1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-lactamase CTX-M-9 (Fragment).
GN BLACTX-M-9.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=743-D;
RA Sabate M., Navarro F., Miro E., Campoy S., Mirelis B., Barbe J.,
RA Prats G.;
RT "A novel complex sull-type integron in Escherichia coli carrying the
RT bla(CTX-M-9) gene."
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY092058; AAM15718.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1071 MW; C26BF418D050440D CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 4 AR 5

RESULT 6

P77404

ID P77404 PRELIMINARY; PRT; 11 AA.
AC P77404;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE DNA sequence downstream of the ECOPRRI HSD locus (Fragment).
GN HSDR.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97206151; PubMed=9157244;
 RA Tyndall C., Lehnherr H., Sandmeier U., Kulik E., Bickle T.A.;
 RT "The type IC hsd loci of the enterobacteria are flanked by DNA with
 RT high homology to the phage P1 genome: implications for the evolution
 RT and spread of DNA restriction systems.";
 RL Mol. Microbiol. 23:729-736(1997).
 DR EMBL; X98145; CAA66840.1; -.
 DR EMBL; X98144; CAA66839.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1259 MW; 714AB092A4072734 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KS 9
 ||
 Db 1 KS 2

RESULT 7

Q8RMI8

ID Q8RMI8 PRELIMINARY; PRT; 11 AA.
 AC Q8RMI8;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE ErmB (Fragment).
 GN ERMB.
 OS Enterococcus hirae.
 OG Plasmid pMKH1.
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1354;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Borgen K., Sorum M., Wasteson Y., Kruse H., Oppegaard H.;
 RT "Genetic linkage between ermB and vanA in Enterococcus hirae of
 RT poultry origin.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF493942; AAM18554.1; -.
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 KW Plasmid.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1359 MW; 08A7A8AA49C7273B CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3
 ||
 Db 10 RK 11

RESULT 8

Q9K332

ID Q9K332 PRELIMINARY; PRT; 11 AA.
 AC Q9K332;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Geh (Fragment).
 GN GEH.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VARIOUS STRAINS;
 RX MEDLINE=20187516; PubMed=10722640;
 RA Cramton S.E., Schnell N.F., Gotz F., Bruckner R.;
 RT "Identification of a new repetitive element in Staphylococcus
 RT aureus.";
 RL Infect. Immun. 68:2344-2348(2000).
 DR EMBL; AF195967; AAF60251.1; -.
 DR EMBL; AF195963; AAF60243.1; -.
 DR EMBL; AF195964; AAF60245.1; -.
 DR EMBL; AF195965; AAF60247.1; -.
 DR EMBL; AF195966; AAF60249.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1262 MW; 4F978F86AAB1A723 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KT 4
 ||
 Db 1 KT 2

RESULT 9

Q47345

ID Q47345 PRELIMINARY; PRT; 11 AA.
 AC Q47345;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Leader peptide.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RA Faber F., van Giezen M., Van Gorcom R.F.M., Harder W.;
 RT "Identification of two Escherichia coli K12 proteins which are induced
 RT in response to pollutant stress.";
 RL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
 RN [2]

RP SEQUENCE OF 2-11 FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=85134883; PubMed=6396419;
 RA Hudson G.S., Davidson B.E.;
 RT "Nucleotide sequence and transcription of the phenylalanine and
 RT tyrosine operons of Escherichia coli K12.";
 RL J. Mol. Biol. 180:1023-1051(1984).
 DR EMBL; Z70523; CAA94435.1; -.
 SQ SEQUENCE 11 AA; 1402 MW; 87AB199204141775 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RE 6
 ||
 Db 7 RE 8

RESULT 10

Q9R872

ID Q9R872 PRELIMINARY; PRT; 11 AA.
 AC Q9R872;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Dihydrofolate reductase (Fragment).
 GN DFR1.
 OS Escherichia coli.
 OG Plasmid r483.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON=Tn7;
 RA Hansson K., Sundstrom L., Pelletier A., Roy P.H.;
 RT "Sequence and function of the second type of integron in Tn7.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON=Tn7;
 RX MEDLINE=82220022; PubMed=6283361;
 RA Lichtenstein C., Brenner S.;
 RT "Unique insertion site of Tn7 in the E. coli chromosome.";
 RL Nature 297:601-603(1982).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON=Tn7;
 RX MEDLINE=83290694; PubMed=6411680;
 RA Simonsen C.C., Chen E.Y., Levinson A.D.;
 RT "Identification of the type I trimethoprim-resistant dihydrofolate
 RT reductase specified by the Escherichia coli R-plasmid R483: Comparison
 RT with procaryotic and eucaryotic dihydrofolate reductases.";
 RL J. Bacteriol. 155:1001-1008(1983).
 RN [4]
 RP SEQUENCE FROM N.A.

RC TRANSPOSON=Tn7;
RX MEDLINE=83272957; PubMed=6308574;
RA Fling M.E., Richards C.;
RT "The nucleotide sequence of the trimethoprim-resistant dihydrofolate
RT reductase gene harbored by Tn7.";
RL Nucleic Acids Res. 11:5147-5158(1983).
DR EMBL; AJ001816; CAA05032.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1221 MW; 92014864C2C69735 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SK 10
||
Db 10 SK 11

RESULT 11

Q91UY9

ID Q91UY9 PRELIMINARY; PRT; 11 AA.
AC Q91UY9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Insertion site for insertion element IS903.B, upstream of kanamycin
DE resistance gene (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSPOSON=Tn2680;
RX MEDLINE=85234397; PubMed=2989253;
RA Mollet B., Clerget M., Meyer J., Iida S.;
RT "Organization of the Tn6-related kanamycin resistance transposon
RT Tn2680 carrying two copies of IS26 and an IS903 variant, IS903.B.";
RL J. Bacteriol. 163:55-60(1985).
DR EMBL; M11420; AAA27427.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1278 MW; 03902598AB0416D0 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RE 6
||
Db 6 RE 7

RESULT 12

Q9C1R7

ID Q9C1R7 PRELIMINARY; PRT; 11 AA.
AC Q9C1R7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ssulp (Fragment).
GN SSU1.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T73;
RA Perez-Ortin J.E.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF239758; AAK15080.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1274 MW; 12567614D732D374 CRC64;

Query Match 18.2%; Score 2; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TR 5
||
Db 10 TR 11

RESULT 13 Q14759

ID Q14759 PRELIMINARY; PRT; 11 AA.
AC Q14759;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Lymphocyte cytosolic protein 2 (Fragment).
GN LCP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sunden S.L.F., Carr L.L., Clements J.L, Motto D.G., Koretzky G.A.;
RT "Polymorphism in and localization of the gene encoding the 76 kDa SH2
RT domain-containing Leukocyte Protein (SLP-76) to chromosome 5q33.1-
RT qter.";
RL Genomics 0:0-0(1995).
DR EMBL; U44065; AAA93308.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1242 MW; D695104224072DDD CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3
||
Db 7 RK 8

RESULT 14

Q9Y3G2

ID Q9Y3G2 PRELIMINARY; PRT; 11 AA.
AC Q9Y3G2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE LSFR2 protein (Fragment).
GN LSFR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99299247; PubMed=10369878;
RA Gilley J., Fried M.;
RT "Extensive gene order differences within regions of conserved synteny
RT between the Fugu and human genomes: implications for chromosomal
RT volution and the cloning of disease genes.";
RL Hum. Mol. Genet. 8:1313-1320(1999).
DR EMBL; Y17456; CAB44349.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1342 MW; 68C5E5D7A8772324 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3
||
Db 4 RK 5

RESULT 15

Q16427

ID Q16427 PRELIMINARY; PRT; 11 AA.
AC Q16427;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Dystrophin protein (Fragment).
GN DYSTROPHIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163501; PubMed=8566960;

RA Holder E., Maeda M., Bies R.D.;
 RT "Expression and regulation of the dystrophin Purkinje promoter in
 RT human skeletal muscle, heart, and brain."
 RL Hum. Genet. 97:232-239(1996).
 DR EMBL; S81419; AAD14362.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1299 MW; DDCC84321AB5A5A2 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ER 7
 ||
 Db 8 ER 9

RESULT 16

Q9UCP5

ID Q9UCP5 PRELIMINARY; PRT; 11 AA.
 AC Q9UCP5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Aggrecan core protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92235266; PubMed=1569188;
 RA Sandy J.D., Flannery C.R., Neame P.J., Lohmander L.S.;
 RL J. Clin. Invest. 89:1512-1516(1992).
 DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
 DR GO; GO:0001501; P:skeletal development; NAS.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1149 MW; 8FBFE8DFE72042D5 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
 ||
 Db 1 AR 2

RESULT 17

Q9UC46

ID Q9UC46 PRELIMINARY; PRT; 11 AA.
 AC Q9UC46;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Neutrophil inhibitor peptide, NIP=POLYMORPHONUCLEAR neutrophil
 DE inhibitor peptide.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96326114; PubMed=8703476;
 RA Cooper J.A.Jr., Culbreth R.R.;
 RT "Characterization of a neutrophil inhibitor peptide harvested from
 RT human bronchial lavage: homology to influenza A nucleoprotein.";
 RL Am. J. Respir. Cell Mol. Biol. 15:207-215(1996).
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0030236; P:anti-inflammatory response; NAS.
 SQ SEQUENCE 11 AA; 1262 MW; 951A1C3279C9DB45 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RE 6
 ||
 Db 1 RE 2

RESULT 18

Q25916

ID Q25916 PRELIMINARY; PRT; 11 AA.
 AC Q25916;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Malaria antigen (7H8/2) (Fragment).
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91164876; PubMed=1706114;
 RA Limpaboon T., Taylor D., Jones G., Geysen H.M., Saul A.;
 RT "Characterization of a Plasmodium falciparum epitope recognized by a
 RT monoclonal antibody with broad isolate and species specificity.";
 RL Southeast Asian J. Trop. Med. Public Health 21:388-396(1990).
 DR EMBL; M31305; AAA29645.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1415 MW; DB03D3BC42C33699 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KS 9
 ||
 Db 1 KS 2

RESULT 19

Q9NFX0

ID Q9NFX0 PRELIMINARY; PRT; 11 AA.
 AC Q9NFX0;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Mitochondrial aconitase (Fragment).
 GN ACON OR MAC OR CG9244.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CANTON S;
 RA Lind M.I.;
 RT "Charaterisation of two iron regulatory proteins and mitochondrial
 RT aconitase in Drosophila melanogaster."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ252019; CAB93522.1; -.
 DR FlyBase; FBgn0010100; Acon.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1204 MW; 7C889CE4D4469734 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
 ||
 Db 3 AR 4

RESULT 20

Q8MM58

ID Q8MM58 PRELIMINARY; PRT; 11 AA.
 AC Q8MM58;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Mannose phosphate isomerase (Fragment).
 GN MPI.
 OS Heliconius cydno chioneus.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconius.
 OX NCBI_TaxID=171915;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=STRI-B-553-Mpi-1, and STRI-B-553-Mpi-2;
 RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,
 RA Mallet J.;
 RT "Molecular evidence for gene flow between species of Heliconius."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF516222; AAM61908.1; -.

DR EMBL; AF516223; AAM61909.1; -.
 DR GO; GO:0016853; F:isomerase activity; IEA.
 KW Isomerase.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1312 MW; 56A67DB31DD1EAA3 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KD 11
 ||
 Db 4 KD 5

RESULT 21

Q95PX6

ID Q95PX6 PRELIMINARY; PRT; 11 AA.
 AC Q95PX6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN ZK1236.8.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium."
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Favello A.;
 RT "The sequence of C. elegans cosmid ZK1236."
 RL Submitted (MAY-1993) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RT "Direct Submission."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; L13200; AAL11108.1; -.
 DR WormPep; ZK1236.8; CE29629.
 KW Hypothetical protein.
 SQ SEQUENCE 11 AA; 1304 MW; DFA3510A25A76322 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SK 10
||
Db 7 SK 8

RESULT 22

Q9TRW5

ID Q9TRW5 PRELIMINARY; PRT; 11 AA.
AC Q9TRW5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 25 kDa protein P25, peptide F4 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=91372400; PubMed=1909972;
RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,
RA Shiratsuchi A., Uchida T., Imahori K.;
RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a
RT Ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions."
RL FEBS Lett. 289:37-43(1991).
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1276 MW; CAF72DAF65A76AA9 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ER 7
||
Db 2 ER 3

RESULT 23

Q9TQS0

ID Q9TQS0 PRELIMINARY; PRT; 11 AA.
AC Q9TQS0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE C-KIT (Fragment).
GN KIT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Olsen H.G., Vage D.I., Lien S., Klungland H.;

RT "A polymorphism in the bovine c-kit gene.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ243424; CAB60775.1; -.
 DR EMBL; AJ243060; CAB60774.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1126 MW; DD785FF8A2D2D772 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SK 10
 ||
 Db 10 SK 11

RESULT 24

O78119

ID O78119 PRELIMINARY; PRT; 11 AA.
 AC O78119;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 1 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050017; AAC41356.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1276 MW; 03C12D8AB2CDCB54 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
 ||
 Db 8 TR 9

RESULT 25

O77911

ID O77911 PRELIMINARY; PRT; 11 AA.
 AC O77911;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 3 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050022; AAC41361.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1401 MW; 74342D9002D41B5B CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ER 7
 ||
 Db 8 ER 9

RESULT 26

O77908

ID O77908 PRELIMINARY; PRT; 11 AA.
 AC O77908;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 2 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050019; AAC41358.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1261 MW; 4346CE9A7EB69EB3 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SK 10
||
Db 3 SK 4

RESULT 27

O77893

ID O77893 PRELIMINARY; PRT; 11 AA.
AC O77893;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 10 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
class II B loci."
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050003; AAC41342.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1296 MW; 68775B73786B572B CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RE 6
||
Db 3 RE 4

RESULT 28

Q94V94

ID Q94V94 PRELIMINARY; PRT; 11 AA.
AC Q94V94;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus storri.

OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
 OX NCBI_TaxID=169855;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL; AF407531; AAL10145.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1387 MW; 8CBDEE80C7336411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TR 5
 ||
 Db 4 TR 5

RESULT 29

Q9G646

ID Q9G646 PRELIMINARY; PRT; 11 AA.
 AC Q9G646;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Sitana ponticeriana.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Sitana.
 OX NCBI_TaxID=118235;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128481; AAG00680.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.

FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1355 MW; 0A2D371E336411A0 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 5 TR 6

RESULT 30

Q9G5W2

ID Q9G5W2 PRELIMINARY; PRT; 11 AA.
AC Q9G5W2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Laudakia tuberculata.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;
OC Laudakia.
OX NCBI_TaxID=118215;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128514; AAG00779.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1327 MW; A8F7371E336411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 5 TR 6

RESULT 31

Q9G631

ID Q9G631 PRELIMINARY; PRT; 11 AA.
 AC Q9G631;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Calotes nigrilabris.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Calotes.
 OX NCBI_TaxID=118098;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128486; AAG00695.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
 ||
 Db 5 TR 6

RESULT 32

Q9G622

ID Q9G622 PRELIMINARY; PRT; 11 AA.
 AC Q9G622;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Salea horsfieldii.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Salea.
 OX NCBI_TaxID=118233;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128490; AAG00707.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1264 MW; 5B2C371E33640DD7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
 ||
 Db 5 AR 6

RESULT 33

Q94VG8

ID Q94VG8 PRELIMINARY; PRT; 11 AA.
 AC Q94VG8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Varanus gouldii (Gould's monitor).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
 OX NCBI_TaxID=62042;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL; AF407502; AAL10060.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1370 MW; 8E6DEE80C7336411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 4 TR 5

RESULT 34

Q9G365

ID Q9G365 PRELIMINARY; PRT; 11 AA.
AC Q9G365;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Calotes emma.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Calotes.
OX NCBI_TaxID=52214;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153820; PubMed=9000751;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Replication slippage may cause parallel evolution in the secondary
RT structures of mitochondrial transfer RNAs."
RL Mol. Biol. Evol. 14:30-39(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards."
RL Syst. Biol. 49:257-277(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics."
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128487; AAG00698.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 5 TR 6

RESULT 35

Q9G5Y6

ID Q9G5Y6 PRELIMINARY; PRT; 11 AA.
AC Q9G5Y6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Agama agama (Red-headed rock agama).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae; Agama.
OX NCBI_TaxID=103336;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128504; AAG00749.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1324 MW; 9D52EC1E336415A1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KT 4
||
Db 3 KT 4

RESULT 36

Q8MEL7

ID Q8MEL7 PRELIMINARY; PRT; 11 AA.
AC Q8MEL7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).

GN RPL16.
 OS *Sida hookeriana*.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; *Sida*.
 OX NCBI_TaxID=108446;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of *Hibiscus* and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of *ndhF* and the *rpl16* intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384624; AAM50396.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
 ||
 Db 3 TR 4

RESULT 37

Q9G5Y0

ID Q9G5Y0 PRELIMINARY; PRT; 11 AA.
 AC Q9G5Y0;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS *Pseudotrapelus sinaitus*.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;
 OC *Pseudotrapelus*.
 OX NCBI_TaxID=118229;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard

RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128507; AAG00758.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1374 MW; B05439FE336415B6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SK 10
 ||
 Db 2 SK 3

RESULT 38

Q9G5W5

ID Q9G5W5 PRELIMINARY; PRT; 11 AA.
 AC Q9G5W5;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Laudakia nupta.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;
 OC Laudakia.
 OX NCBI_TaxID=118212;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128513; AAG00776.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1361 MW; A8F73710D36411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 5 TR 6

RESULT 39

Q9G607

ID Q9G607 PRELIMINARY; PRT; 11 AA.
AC Q9G607;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Aphaniotis fusca.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Aphaniotis.
OX NCBI_TaxID=89036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128495; AAG00722.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1389 MW; A68E371E336411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 5 TR 6

RESULT 40

Q94V77

ID Q94V77 PRELIMINARY; PRT; 11 AA.
AC Q94V77;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Heloderma suspectum (Gila monster).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;
 OC Heloderma.
 OX NCBI_TaxID=8554;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL; AF407540; AAL10172.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1396 MW; 8E3A6DE0D5A36411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
 ||
 Db 4 TR 5

RESULT 41

Q9G628

ID Q9G628 PRELIMINARY; PRT; 11 AA.
 AC Q9G628;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Calotes mystaceus.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Calotes.
 OX NCBI_TaxID=118097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics.";

RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128488; AAG00701.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TR 5
 ||
 Db 5 TR 6

RESULT 42

O79985

ID O79985 PRELIMINARY; PRT; 11 AA.
 AC O79985;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome C oxidase subunit I (Fragment).
 GN COI.
 OS laudakia caucasia.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;
 OC laudakia.
 OX NCBI_TaxID=71145;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98424476; PubMed=9751922;
 RA Macey J.R., Schulte J.A. II, Ananjeva N.B., Larson A.,
 RA Rastegar-Pouyani N., Shammakov S.M., Papenfuss T.J.;
 RT "Phylogenetic relationships among Agamid lizards of the Laudakia
 RT caucasia species group: testing hypotheses of biogeographic
 RT fragmentation and an area cladogram for the Iranian Plateau."
 RL Mol. Phylogenet. Evol. 10:118-131(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20179532; PubMed=10712852;
 RA Macey J.R., Schulte J.A. II, Kami H.G., Ananjeva N.B., Larson A.,
 RA Papenfuss T.J.;
 RT "Testing hypotheses of vicariance in the agamid lizard laudakia
 RT caucasia from mountain ranges on the northern iranain plateau."
 RL Mol. Phylogenet. Evol. 14:479-483(2000).
 DR EMBL; AF028687; AAC99614.1; -.
 DR EMBL; AF028681; AAC99596.1; -.
 DR EMBL; AF028682; AAC99599.1; -.
 DR EMBL; AF028683; AAC99602.1; -.
 DR EMBL; AF028684; AAC99605.1; -.
 DR EMBL; AF028685; AAC99608.1; -.
 DR EMBL; AF028686; AAC99611.1; -.
 DR EMBL; AF172705; AAF65208.1; -.
 DR EMBL; AF172704; AAF65205.1; -.

DR PIR; T12264; T12264.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1361 MW; A8F73710D36411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 5 TR 6

RESULT 43

Q94VI5

ID Q94VI5 PRELIMINARY; PRT; 11 AA.
AC Q94VI5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus exanthematicus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=8557;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407496; AAL10043.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1382 MW; 8A26C780C7336411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 4 TR 5

RESULT 44

Q9G359

ID Q9G359 PRELIMINARY; PRT; 11 AA.
AC Q9G359;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).

GN COI.
 OS Japalura flaviceps.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Japalura.
 OX NCBI_TaxID=52218;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97153820; PubMed=9000751;
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Replication slippage may cause parallel evolution in the secondary
 RT structures of mitochondrial transfer RNAs.";
 RL Mol. Biol. Evol. 14:30-39(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128500; AAG00737.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1341 MW; 538E371E33640DD7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
 ||
 Db 5 AR 6

RESULT 45

Q8MEM2

ID Q8MEM2 PRELIMINARY; PRT; 11 AA.
 AC Q8MEM2;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Lagunaria patersonia.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Malvales; Malvaceae; Malvoideae; Lagunaria.
 OX NCBI_TaxID=183274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384616; AAM50388.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
 ||
 Db 3 TR 4

RESULT 46

Q9G649

ID Q9G649 PRELIMINARY; PRT; 11 AA.
 AC Q9G649;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Otocryptis wiegmanni.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Otocryptis.
 OX NCBI_TaxID=118220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards."
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics."
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128480; AAG00677.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.

FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1347 MW; 932D3710D3640DC1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 5 AR 6

RESULT 47

Q9G643

ID Q9G643 PRELIMINARY; PRT; 11 AA.
AC Q9G643;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Calotes calotes.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Calotes.
OX NCBI_TaxID=118093;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128482; AAG00683.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1373 MW; BE2D371E336411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 5 TR 6

RESULT 48

Q9G5X4

ID Q9G5X4 PRELIMINARY; PRT; 11 AA.
 AC Q9G5X4;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS *Trapelus agilis*.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;
 OC *Trapelus*.
 OX NCBI_TaxID=52210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards."
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics."
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128509; AAG00764.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1391 MW; BFC73710D36411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
 ||
 Db 5 TR 6

RESULT 49

Q94V74

ID Q94V74 PRELIMINARY; PRT; 11 AA.
 AC Q94V74;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS *Lanthanotus borneensis*.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Lanthanotidae;
 OC Lanthanotus.
 OX NCBI_TaxID=62058;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL; AF407541; AAL10175.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1388 MW; 8F28EE80C7336411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
 ||
 Db 4 TR 5

RESULT 50

Q8MES5

ID Q8MES5 PRELIMINARY; PRT; 11 AA.
 AC Q8MES5;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Abelmoschus manihot.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Abelmoschus.
 OX NCBI_TaxID=183220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384561; AAM50399.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
 ||

Db

3 TR 4

RESULT 51

Q9G616

ID Q9G616 PRELIMINARY; PRT; 11 AA.
 AC Q9G616;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Ceratophora stoddartii.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Ceratophora.
 OX NCBI_TaxID=118196;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21655505; PubMed=11796034;
 RA Schulte J.A. II, Macey J.R., Pethiyagoda R., Larson A.;
 RT "Rostral Horn Evolution among Agamid Lizards of the Genus Ceratophora
 RT Endemic to Sri Lanka.";
 RL Mol. Phylogenet. Evol. 22:111-117(2002).
 DR EMBL; AF128492; AAG00713.1; -.
 DR EMBL; AF364054; AAL68027.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1295 MW; 5B2C371E336411A7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5

||

Db 5 TR 6

RESULT 52

Q9G350

ID Q9G350 PRELIMINARY; PRT; 11 AA.
AC Q9G350;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Laudakia sacra.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;
OC Laudakia.
OX NCBI_TaxID=52204;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153820; PubMed=9000751;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Replication slippage may cause parallel evolution in the secondary
RT structures of mitochondrial transfer RNAs.";
RL Mol. Biol. Evol. 14:30-39(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128515; AAG00782.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1361 MW; A8F73710D36411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 5 TR 6

RESULT 53

Q9G610

ID Q9G610 PRELIMINARY; PRT; 11 AA.
AC Q9G610;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Lyriocephalus scutatus.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Lyriocephalus.
 OX NCBI_TaxID=118218;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21655505; PubMed=11796034;
 RA Schulte J.A. II, Macey J.R., Pethiyagoda R., Larson A.;
 RT "Rostral Horn Evolution among Agamid Lizards of the Genus Ceratophora
 RT Endemic to Sri Lanka.";
 RL Mol. Phylogenet. Evol. 22:111-117(2002).
 DR EMBL; AF128494; AAG00719.1; -.
 DR EMBL; AF364052; AAL68021.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1295 MW; 5B2C371E336411A7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
 ||
 Db 5 TR 6

RESULT 54
 079636

ID 079636 PRELIMINARY; PRT; 11 AA.
 AC 079636;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Laudakia himalayana.

OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;
 OC Laudakia.
 OX NCBI_TaxID=71147;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98424476; PubMed=9751922;
 RA Macey J.R., Schulte J.A. II, Ananjeva N.B., Larson A.,
 RA Rastegar-Pouyani N., Shammakov S.M., Papenfuss T.J.;
 RT "Phylogenetic relationships among Agamid lizards of the Laudakia
 RT caucasia species group: testing hypotheses of biogeographic
 RT fragmentation and an area cladogram for the Iranian Plateau.";
 RL Mol. Phylogenet. Evol. 10:118-131(1998).
 DR EMBL; AF028676; AAC99581.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1296 MW; 85F7371E336411B1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
 ||
 Db 5 TR 6

RESULT 55

Q9G5Z8

ID Q9G5Z8 PRELIMINARY; PRT; 11 AA.
 AC Q9G5Z8;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Acanthosaura lepidogaster.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Acanthosaura.
 OX NCBI_TaxID=118088;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard

RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128499; AAG00734.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1279 MW; 5DF7371E33640DD7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
 ||
 Db 5 AR 6

RESULT 56

Q9G5W8

ID Q9G5W8 PRELIMINARY; PRT; 11 AA.
 AC Q9G5W8;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Trapelus savignyi.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;
 OC Trapelus.
 OX NCBI_TaxID=118240;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128512; AAG00773.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1361 MW; A8F73710D36411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 5 TR 6

RESULT 57

Q8MEP0

ID Q8MEP0 PRELIMINARY; PRT; 11 AA.
AC Q8MEP0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Hibiscus peralbus.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
OX NCBI_TaxID=183256;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron."
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384598; AAM50370.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 3 TR 4

RESULT 58

Q8MER8

ID Q8MER8 PRELIMINARY; PRT; 11 AA.
AC Q8MER8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Dombeya tiliacea.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Dombeyoideae; Dombeya.
OX NCBI_TaxID=121875;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384569; AAM50407.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1424 MW; 7227C351D32AE9D4 CRC64;

 Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 4 TR 5
 ||
 Db 3 TR 4

RESULT 59

Q9G5V3
 ID Q9G5V3 PRELIMINARY; PRT; 11 AA.
 AC Q9G5V3;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Phrynocephalus mystaceus.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;
 OC Phrynocephalus.
 OX NCBI_TaxID=116118;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128518; AAG00791.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1343 MW; 5DF73710D36411A7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 5 TR 6

RESULT 60

Q94VE7

ID Q94VE7 PRELIMINARY; PRT; 11 AA.
AC Q94VE7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus komodoensis (Komodo dragon).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=61221;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407510; AAL10084.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1370 MW; 8E6DEE80C7336411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 4 TR 5

RESULT 61

Q8WES0

ID Q8WES0 PRELIMINARY; PRT; 11 AA.
AC Q8WES0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Ceratophora karu.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;

OC Ceratophora.
 OX NCBI_TaxID=118086;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and phylogenetic information content of mitochondrial
 RT genomic structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21655505; PubMed=11796034;
 RA Schulte J.A. II, Macey J.R., Pethiyagoda R., Larson A.;
 RT "Rostral Horn Evolution among Agamid Lizards of the Genus Ceratophora
 RT Endemic to Sri Lanka.";
 RL Mol. Phylogenet. Evol. 22:111-117(2002).
 DR EMBL; AF128520; AAL67604.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
 ||
 Db 5 TR 6

RESULT 62

Q94VB8

ID Q94VB8 PRELIMINARY; PRT; 11 AA.
 AC Q94VB8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Varanus salvadorii (Crocodile monitor).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
 OX NCBI_TaxID=62049;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL; AF407522; AAL10119.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1370 MW; 8E6DEE80C7336411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 4 TR 5

RESULT 63

Q9G634

ID Q9G634 PRELIMINARY; PRT; 11 AA.
AC Q9G634;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Calotes liolepis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Calotes.
OX NCBI_TaxID=118096;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128485; AAG00692.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 5 TR 6

RESULT 64

Q9G353

ID Q9G353 PRELIMINARY; PRT; 11 AA.
AC Q9G353;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Trapelus sanguinolentus.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;
 OC Trapelus.
 OX NCBI_TaxID=118238;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97153820; PubMed=9000751;
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Replication slippage may cause parallel evolution in the secondary
 RT structures of mitochondrial transfer RNAs.";
 RL Mol. Biol. Evol. 14:30-39(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128511; AAG00770.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1361 MW; A8F73710D36411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
 ||
 Db 5 TR 6

RESULT 65

079642

ID 079642 PRELIMINARY; PRT; 11 AA.
 AC 079642;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.

OS *Laudakia microlepis*.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;
 OC *Laudakia*.
 OX NCBI_TaxID=71149;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98424476; PubMed=9751922;
 RA Macey J.R., Schulte J.A. II, Ananjeva N.B., Larson A.,
 RA Rastegar-Pouyani N., Shammakov S.M., Papenfuss T.J.;
 RT "Phylogenetic relationships among Agamid lizards of the *Laudakia*
 RT *caucasia* species group: testing hypotheses of biogeographic
 RT fragmentation and an area cladogram for the Iranian Plateau."
 RL Mol. Phylogenet. Evol. 10:118-131(1998).
 DR EMBL; AF028678; AAC99587.1; -.
 DR PIR; T12248; T12248.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1327 MW; A8F7371E336411A6 CRC64;

 Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 4 TR 5
 ||
 Db 5 TR 6

RESULT 66

Q8MES1
 ID Q8MES1 PRELIMINARY; PRT; 11 AA.
 AC Q8MES1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS *Alyogyne pinoniana*.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; *Alyogyne*.
 OX NCBI_TaxID=183226;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of *Hibiscus* and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of *ndhF* and the *rpl16* intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384566; AAM50404.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 3 TR 4

RESULT 67

Q94VH7

ID Q94VH7 PRELIMINARY; PRT; 11 AA.
AC Q94VH7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus gilleni (Pygmy mulga monitor).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169840;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407499; AAL10051.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1340 MW; CF6DEE80C733640D CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 4 AR 5

RESULT 68

Q8SKR0

ID Q8SKR0 PRELIMINARY; PRT; 11 AA.
AC Q8SKR0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Rankinia diemensis (Mountain dragon).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
 OC Rankinia.
 OX NCBI_TaxID=180914;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21623804; PubMed=11754013;
 RA Melville J., Schulte J.A. II, Larson A.;
 RT "A molecular phylogenetic study of ecological diversification in the
 RT Australian lizard genus Ctenophorus.";
 RL J. Exp. Zool. 291:339-353(2001).
 DR EMBL; AF375619; AAL78779.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1340 MW; B405371E336411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
 ||
 Db 5 TR 6

RESULT 69

Q9G601

ID Q9G601 PRELIMINARY; PRT; 11 AA.
 AC Q9G601;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Bronchocela cristatella (Green crested lizard).
 OG Mitochondrion..
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Bronchocela.
 OX NCBI_TaxID=118090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128497; AAG00728.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 5 TR 6

RESULT 70

Q8MEP3

ID Q8MEP3 PRELIMINARY; PRT; 11 AA.
AC Q8MEP3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Hibiscus normanii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
OX NCBI_TaxID=183253;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384595; AAM50367.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 3 TR 4

RESULT 71

Q9G619

ID Q9G619 PRELIMINARY; PRT; 11 AA.
AC Q9G619;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Ceratophora aspera.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Ceratophora.
 OX NCBI_TaxID=118195;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards."
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics."
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128491; AAG00710.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1264 MW; 5B2C371E33640DD7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
 ||
 Db 5 AR 6

RESULT 72

Q8WER7

ID Q8WER7 PRELIMINARY; PRT; 11 AA.
 AC Q8WER7;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Ceratophora tennentii.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Ceratophora.
 OX NCBI_TaxID=118087;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;

RT "Evolution and phylogenetic information content of mitochondrial
 RT genomic structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21655505; PubMed=11796034;
 RA Schulte J.A. II, Macey J.R., Pethiyagoda R., Larson A.;
 RT "Rostral Horn Evolution among Agamid Lizards of the Genus Ceratophora
 RT Endemic to Sri Lanka.";
 RL Mol. Phylogenet. Evol. 22:111-117(2002).
 DR EMBL; AF128521; AAL67607.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1264 MW; 5B2C371E33640DD7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
 ||
 Db 5 AR 6

RESULT 73

Q8WD50

ID Q8WD50 PRELIMINARY; PRT; 11 AA.
 AC Q8WD50;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Ceratophora stoddartii.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Ceratophora.
 OX NCBI_TaxID=118196;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21655505; PubMed=11796034;
 RA Schulte J.A. II, Macey J.R., Pethiyagoda R., Larson A.;
 RT "Rostral Horn Evolution among Agamid Lizards of the Genus Ceratophora
 RT Endemic to Sri Lanka.";
 RL Mol. Phylogenet. Evol. 22:111-117(2002).
 DR EMBL; AF364053; AAL68024.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1264 MW; 5B2C371E33640DD7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
||
Db 5 AR 6

RESULT 74

Q94VK1

ID Q94VK1 PRELIMINARY; PRT; 11 AA.
AC Q94VK1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus acanthurus (Ridge-tailed monitor).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62035;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407488; AAL10021.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1370 MW; 8E6DEE80C7336411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
||
Db 4 TR 5

RESULT 75

Q9G5X7

ID Q9G5X7 PRELIMINARY; PRT; 11 AA.
AC Q9G5X7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Trapelus ruderatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;
OC Trapelus.
OX NCBI_TaxID=118237;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;

RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128508; AAG00761.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1309 MW; 5DF7371E336411A7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TR 5
 ||
 Db 5 TR 6

Search completed: April 8, 2004, 15:46:07
 Job time : 28.7692 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 5.15385 Seconds
 (without alignments)
 111.135 Million cell updates/sec

Title: US-09-787-443A-14
 Perfect score: 11
 Sequence: 1 ARKTRERKSKD 11

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 70

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8							
Result	Query						
No.	Score	Match	Length	DB	ID		Description
1	3	27.3	11	1	TKN_ELEMO	P01293	eledone mos
2	3	27.3	11	1	UXB2_YEAST	P99013	saccharomyc
3	2	18.2	11	1	BRK_MEGFL	P12797	megascolia
4	2	18.2	11	1	ES1_RAT	P56571	rattus norv
5	2	18.2	11	1	MORN_HUMAN	P01163	homo sapien
6	2	18.2	11	1	Q20A_COMTE	P80464	comamonas t
7	2	18.2	11	1	RR2_CONAM	P42341	conopholis
8	2	18.2	11	1	RS30_ONCMY	P83328	oncorhynchu
9	2	18.2	11	1	TKN2_UPERU	P08616	uperoleia r
10	2	18.2	11	1	TKNA_RANRI	P29207	rana ridibu
11	2	18.2	11	1	TKND_RANCA	P22691	rana catesb
12	1	9.1	11	1	ANGT_CRIGE	P09037	crinia geor
13	1	9.1	11	1	ASL1_BACSE	P83146	bacteroides
14	1	9.1	11	1	ASL2_BACSE	P83147	bacteroides
15	1	9.1	11	1	BPP3_BOTIN	P30423	bothrops in
16	1	9.1	11	1	BPP4_BOTIN	P30424	bothrops in
17	1	9.1	11	1	BPPB_AGKHA	P01021	agkistrodon

18	1	9.1	11	1	BPP_AGKHP	P04562	agkistrodon
19	1	9.1	11	1	CA21_LITCI	P82087	litoria cit
20	1	9.1	11	1	CA22_LITCI	P82088	litoria cit
21	1	9.1	11	1	CA31_LITCI	P82089	litoria cit
22	1	9.1	11	1	CA32_LITCI	P82090	litoria cit
23	1	9.1	11	1	CA41_LITCI	P82091	litoria cit
24	1	9.1	11	1	CA42_LITCI	P82092	litoria cit
25	1	9.1	11	1	CEP1_ACHFU	P22790	achatina fu
26	1	9.1	11	1	CORZ_PERAM	P11496	periplaneta
27	1	9.1	11	1	COXA_CANFA	P99501	canis famil
28	1	9.1	11	1	CSI5_BACSU	P81095	bacillus su
29	1	9.1	11	1	CX5A_CONAL	P58848	conus aulic
30	1	9.1	11	1	CX5B_CONAL	P58849	conus aulic
31	1	9.1	11	1	CXL1_CONMR	P58807	conus marmo
32	1	9.1	11	1	EFG_CLOPA	P81350	clostridium
33	1	9.1	11	1	FAR6_PENMO	P83321	penaeus mon
34	1	9.1	11	1	FAR9_CALVO	P41864	calliphora
35	1	9.1	11	1	HS70_PINPS	P81672	pinus pinas
36	1	9.1	11	1	LADD_ONCMY	P81018	oncorhynch
37	1	9.1	11	1	LPW_THETH	P05624	thermus the
38	1	9.1	11	1	LSK1_LEUMA	P04428	leucophaea
39	1	9.1	11	1	LSKP_PERAM	P36885	periplaneta
40	1	9.1	11	1	MHBI_KLEPN	P80580	klebsiella
41	1	9.1	11	1	MLG_THETS	P41989	theromyzon
42	1	9.1	11	1	NUHM_CANFA	P49820	canis famil
43	1	9.1	11	1	NXSN_PSETE	P59072	pseudonaja
44	1	9.1	11	1	OAIF_SARBU	P83518	sarcophaga
45	1	9.1	11	1	PKC1_CARMO	P82684	carausius m
46	1	9.1	11	1	PQQC_PSEFL	P55173	pseudomonas
47	1	9.1	11	1	PVK1_PERAM	P41837	periplaneta
48	1	9.1	11	1	RANC_RANPI	P08951	rana pipien
49	1	9.1	11	1	RE41_LITRU	P82074	litoria rub
50	1	9.1	11	1	RRPL_CHAV	P13179	chandipura
51	1	9.1	11	1	T2P1_PROVU	P31031	proteus vul
52	1	9.1	11	1	TIN1_HOPTI	P82651	hoplobatr
53	1	9.1	11	1	TIN4_HOPTI	P82654	hoplobatr
54	1	9.1	11	1	TKC2_CALVO	P41518	calliphora
55	1	9.1	11	1	TKN1_PSEGU	P42986	pseudophryn
56	1	9.1	11	1	TKN1_UPEIN	P82026	uperoleia i
57	1	9.1	11	1	TKN1_UPERU	P08612	uperoleia r
58	1	9.1	11	1	TKN2_PSEGU	P42987	pseudophryn
59	1	9.1	11	1	TKN3_PSEGU	P42988	pseudophryn
60	1	9.1	11	1	TKN4_PSEGU	P42989	pseudophryn
61	1	9.1	11	1	TKN5_PSEGU	P42990	pseudophryn
62	1	9.1	11	1	TKNA_CHICK	P19850	gallus gall
63	1	9.1	11	1	TKNA_GADMO	P28498	gadus morhu
64	1	9.1	11	1	TKNA_HORSE	P01290	equus cabal
65	1	9.1	11	1	TKNA_ONCMY	P28499	oncorhynch
66	1	9.1	11	1	TKNA_RANCA	P22688	rana catesb
67	1	9.1	11	1	TKNA_SCYCA	P41333	scyliorhinu
68	1	9.1	11	1	TKN_PHYFU	P08615	physalaemus
69	1	9.1	11	1	UF05_MOUSE	P38643	mus musculu
70	1	9.1	11	1	ULAG_HUMAN	P31933	homo sapien

ALIGNMENTS

RESULT 1

TKN_ELEMO

ID TKN_ELEMO STANDARD; PRT; 11 AA.
AC P01293;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Eledoisin.
OS Eledone moschata (Musky octopus) (Ozaena moschata), and
OS Eledone cirrhosa (Curled octopus) (Ozaena cirrosa).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Eledone.
OX NCBI_TaxID=6641, 102876;
RN [1]
RP SEQUENCE.
RA Anastasi A., Erspamer V.;
RT "The isolation and amino acid sequence of eledoisin, the active
RT endecapeptide of the posterior salivary glands of Eledone.";
RL Arch. Biochem. Biophys. 101:56-65(1963).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; A01561; EOOC.
DR PIR; B01561; EOCC.
DR PDB; 1MXQ; 18-FEB-03.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;
KW 3D-structure.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1206 MW; 570D7C2559CDDAA3 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SKD 11
|||
Db 3 SKD 5

RESULT 2

UXB2_YEAST

ID UXB2_YEAST STANDARD; PRT; 11 AA.
AC P99013;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page (Spot 2D-000K2F) (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=X2180-1A;
 RA Sanchez J.-C., Golaz O., Schaller D., Morch F., Frutiger S.,
 RA Hughes G.J., Appel R.D., Deshusses J., Hochstrasser D.F.;
 RL Submitted (AUG-1995) to Swiss-Prot.
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 6.20, its MW is: 9.2 kDa.
 DR SWISS-2DPAGE; P99013; YEAST.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1328 MW; EC38021C0DCB42DA CRC64;

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARK 3
 |||
 Db 7 ARK 9

RESULT 3

BRK_MEGFL
 ID BRK_MEGFL STANDARD; PRT; 11 AA.
 AC P12797;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Megascoliakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like
 DE peptide ([Thr6]bradykinin)].
 OS Megascolia flavifrons (Garden dagger wasp) (Solitary wasp).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Scoliidae; Megascolia.
 OX NCBI_TaxID=7437;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=87293024; PubMed=3617088;
 RA Yasuhara T., Mantel P., Nakajima T., Piek T.;
 RT "Two kinins isolated from an extract of the venom reservoirs of the
 RT solitary wasp Megascolia flavifrons.";
 RL Toxicon 25:527-535(1987).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Nakajima T., Piek T., Yashuara T., Mantel P.;
 RT "Two kinins isolated from the venom of Megascolia flavifrons.";
 RL Toxicon 26:34-34(1988).
 CC -!- FUNCTION: Both proteins have bradykinin-like, although lower
 CC activities (e.g. smooth muscle contraction).
 CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
 CC -!- SIMILARITY: Belongs to the bradykinin family.
 DR PIR; B26744; B26744.
 DR GO; GO:0005615; C:extracellular space; IDA.

DR GO; GO:0045776; P:negative regulation of blood pressure; ISS.
 DR GO; GO:0045987; P:positive regulation of smooth muscle contra. . .; TAS.
 KW Bradykinin; Vasodilator.
 FT PEPTIDE 1 11 MEGASCOLIAKININ.
 FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.
 SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3
 ||
 Db 9 RK 10

RESULT 4

ES1_RAT

ID ES1_RAT STANDARD; PRT; 11 AA.
 AC P56571;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE ES1 protein, mitochondrial (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Wistar; TISSUE=Heart;
 RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
 RA Jungblut P.R.;
 RL Submitted (SEP-1998) to Swiss-Prot.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).
 CC -!- MISCELLANEOUS: By 2D-PAGE, the determined pI of this protein (spot
 CC P2) is: 8.9, its MW is: 25 kDa.
 CC -!- SIMILARITY: BELONGS TO THE ES1 FAMILY.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1142 MW; D862272D32C72DC2 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
 ||
 Db 2 AR 3

RESULT 5

MORN_HUMAN

ID MORN_HUMAN STANDARD; PRT; 11 AA.
 AC P01163;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Morphogenetic neuropeptide (Head activator) (HA).
 OS Homo sapiens (Human),
 OS Rattus norvegicus (Rat),
 OS Bos taurus (Bovine),
 OS Anthopleura elegantissima (Sea anemone), and
 OS Hydra attenuata (Hydra) (Hydra vulgaris).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Human, Rat, and Bovine;
 RX MEDLINE=82035850; PubMed=7290191;
 RA Bodenmuller H., Schaller H.C.;
 RT "Conserved amino acid sequence of a neuropeptide, the head activator,
 RT from coelenterates to humans.";
 RL Nature 293:579-580(1981).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=A.elegantissima, and H.attenuata;
 RA Schaller H.C., Bodenmuller H.;
 RT "Isolation and amino acid sequence of a morphogenetic peptide from
 RT hydra.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
 RN [3]
 RP SYNTHESIS.
 RX MEDLINE=82050803; PubMed=7297679;
 RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;
 RT "Synthesis of a new neuropeptide, the head activator from hydra.";
 RL FEBS Lett. 131:317-321(1981).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=90059923; PubMed=2583101;
 RA Schaller H.C., Druffel-Augustin S., Dubel S.;
 RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells
 RT in the G2/mitosis transition.";
 RL EMBO J. 8:3311-3318(1989).
 CC -!- FUNCTION: HA acts as an autocrine growth factor for neural cells
 CC in the G2/mitosis transition.
 CC -!- CAUTION: This peptide was first isolated from nerve cells of hydra
 CC and was called head activator by the authors, because it induced
 CC head-specific growth and differentiation in this animal. It has
 CC been found in mammalian intestine and hypothalamus.
 DR PIR; A01427; YHRT.
 DR PIR; A93900; YHXAE.
 DR PIR; B01427; YHHU.
 DR PIR; B93900; YHJFHY.
 DR PIR; C01427; YHBO.
 DR GK; P01163; -.
 KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SK 10
 ||
Db 6 SK 7

RESULT 6

Q2OA_COMTE

ID Q2OA_COMTE STANDARD; PRT; 11 AA.
AC P80464;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Quinoline 2-oxidoreductase, alpha chain (EC 1.3.99.17) (Fragment).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Comamonas.
OX NCBI_TaxID=285;
RN [1]
RP SEQUENCE.
RC STRAIN=63;
RX MEDLINE=96035889; PubMed=7556204;
RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;
RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in
RT quinoline and 3-methylquinoline degradation.";
RL Eur. J. Biochem. 232:536-544(1995).
CC -!- FUNCTION: Converts (3-methyl-)-quinoline to (3-methyl-)2-oxo-
CC 1,2-dihydroquinoline.
CC -!- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-
CC 1(2H)-one + reduced acceptor.
CC -!- COFACTOR: FAD, molybdenum and iron-sulfur.
CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)quinoline; first
CC step.
CC -!- SUBUNIT: Heterohexamer of two alpha chains, two beta chains, and
CC two gamma chains (Probable).
DR PIR; S66606; S66606.
KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1213 MW; 869094322B1DC2CA CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KS 9
 ||
Db 2 KS 3

RESULT 7

RR2_CONAM

ID RR2_CONAM STANDARD; PRT; 11 AA.
AC P42341;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Chloroplast 30S ribosomal protein S2 (Fragment).
 GN RPS2.
 OS Conopholis americana (Squawroot).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiids; Lamiales; Orobanchaceae; Orobancheae; Conopholis.
 OX NCBI_TaxID=4179;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92145776; PubMed=1723664;
 RA Taylor G., Wolfe K.H., Morden C.W., Depamphilis C.W., Palmer J.D.;
 RT "Lack of a functional plastid tRNA(Cys) gene is associated with loss
 RT of photosynthesis in a lineage of parasitic plants.";
 RL Curr. Genet. 20:515-518(1991).
 CC -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X64567; CAA45868.1; -.
 DR PIR; S32575; S32575.
 DR HAMAP; MF_00291; -; 1.
 DR InterPro; IPR001865; Ribosomal_S2.
 DR PROSITE; PS00962; RIBOSOMAL_S2_1; PARTIAL.
 DR PROSITE; PS00963; RIBOSOMAL_S2_2; PARTIAL.
 KW Ribosomal protein; Chloroplast.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1497 MW; 76CD719954536B44 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TR 5
 ||
 Db 2 TR 3

RESULT 8

RS30_ONCMY
 ID RS30_ONCMY STANDARD; PRT; 11 AA.
 AC P83328;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 40S ribosomal protein S30 (Fragment).
 GN FAU.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Skin mucus;
 RX MEDLINE=22142142; PubMed=12147245;
 RA Fernandes J.M.O., Smith V.J.;
 RT "A novel antimicrobial function for a ribosomal peptide from rainbow
 RT trout skin.";
 RL Biochem. Biophys. Res. Commun. 296:167-171(2002).
 CC -!- FUNCTION: Has antibacterial activity against Gram-positive
 CC bacteria.
 CC -!- MASS SPECTROMETRY: MW=6676.6; METHOD=MALDI.
 CC -!- SIMILARITY: Belongs to the S30E family of ribosomal proteins.
 KW Ribosomal protein; Antibiotic.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1123 MW; 2312AB630DD735B8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2
 ||
 Db 7 AR 8

RESULT 9

TKN2_UPERU
 ID TKN2_UPERU STANDARD; PRT; 11 AA.
 AC P08616;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Rugosauperolein II ([Lys5,Thr6]physalaemin).
 OS Uperoleia rugosa (Wrinkled toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylaidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=8368;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=80223080; PubMed=7389029;
 RA Nakajima T., Yasuhara T., Erspamer V., Erspamer G.F., Negri L.;
 RT "Physalaemin- and bombesin-like peptides in the skin of the
 RT Australian leptodactylid frog Uperoleia rugosa.";
 RL Chem. Pharm. Bull. 28:689-695(1980).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.

KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1270 MW; 3293693E59D1A327 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KT 4
||
Db 5 KT 6

RESULT 10

TKNA_RANRI
ID TKNA_RANRI STANDARD; PRT; 11 AA.
AC P29207;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranakinin (Substance-P-related peptide).
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92044543; PubMed=1658233;
RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
RT neurokinin B from the brain of the frog Rana ridibunda.";
RL J. Neurochem. 57:2086-2091(1991).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ER 7
||
Db 5 ER 6

RESULT 11

TKND_RANCA

ID TKND_RANCA STANDARD; PRT; 11 AA.
 AC P22691;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranatachykinin D (RTK D).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Intestine;
 RX MEDLINE=91254337; PubMed=2043143;
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
 RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
 RT brain and intestine.";
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=94023216; PubMed=8210506;
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
 RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
 RT intestine.";
 RL Regul. Pept. 46:81-88(1993).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; D61033; D61033.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; FALSE_NEG.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1350 MW; 3A34256C59D40B07 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ER 7
 ||
 Db 5 ER 6

RESULT 12

ANGT_CRIGE

ID ANGT_CRIGE STANDARD; PRT; 11 AA.
 AC P09037;
 DT 01-NOV-1988 (Rel. 09, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Crinia-angiotensin II.
 OS Crinia georgiana (Quacking frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Crinia.
 OX NCBI_TaxID=8374;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=80024575; PubMed=488254;
 RA Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;
 RT "Amino acid composition and sequence of crinia-angiotensin, an
 RT angiotensin II-like endecapeptide from the skin of the Australian
 RT frog Crinia georgiana.";
 RL Experientia 35:1132-1133(1979).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 DR PIR; S07207; S07207.
 KW Vasoconstrictor.
 SQ SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A 1
 |
 Db 1 A 1

RESULT 13

ASL1_BACSE

ID ASL1_BACSE STANDARD; PRT; 11 AA.
 AC P83146;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Acharan sulfate lyase 1 (EC 4.2.2.-) (Fragment).
 OS Bacteroides stercoris.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=46506;
 RN [1]
 RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
 RC STRAIN=HJ-15;
 RX MEDLINE=21223019; PubMed=11322884;
 RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
 RT "Purification and characterization of acharan sulfate lyases, two
 RT novel heparinases, from Bacteroides stercoris HJ-15.";
 RL Eur. J. Biochem. 268:2635-2641(2001).
 CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
 CC heparin and heparan sulfate.
 CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and cobalt.
 CC Activated by reducing agents, such as DL-dithiothreitol and 2-
 CC mercaptoethanol.

CC -!- SUBUNIT: Monomer.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
 CC 7.2 and optimum temperature 45 degrees Celsius.
 KW Lyase; Heparin-binding.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1395 MW; 01B2DAA241E865AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 S 9
 |
 Db 5 S 5

RESULT 14

ASL2_BACSE

ID ASL2_BACSE STANDARD; PRT; 11 AA.
 AC P83147;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Acharan sulfate lyase 2 (EC 4.2.2.-) (Fragment).
 OS Bacteroides stercoris.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=46506;
 RN [1]
 RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
 RC STRAIN=HJ-15;
 RX MEDLINE=21223019; PubMed=11322884;
 RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
 RT "Purification and characterization of acharan sulfate lyases, two
 RT novel heparinases, from Bacteroides stercoris HJ-15."
 RL Eur. J. Biochem. 268:2635-2641(2001).
 CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
 CC heparin and heparan sulfate.
 CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and lead.
 CC Activated by reducing agents, such as DL-dithiothreitol and 2-
 CC mercaptoethanol.
 CC -!- SUBUNIT: Monomer.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
 CC 7.2 and optimum temperature 45 degrees Celsius.
 KW Lyase; Heparin-binding.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1195 MW; D79D897C7AA451AD CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 T 4

Db |
 1 T 1

RESULT 15

BPP3_BOTIN

ID BPP3_BOTIN STANDARD; PRT; 11 AA.
AC P30423;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom."
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; C37196; C37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
 |
Db 6 R 6

RESULT 16

BPP4_BOTIN

ID BPP4_BOTIN STANDARD; PRT; 11 AA.
AC P30424;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.

OX NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom.";
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; D37196; D37196.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1143 MW; 20BBBF13C7741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 R 2
 |
 Db 6 R 6

RESULT 17

BPPB_AGKHA
 ID BPPB_AGKHA STANDARD; PRT; 11 AA.
 AC P01021;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide B (Angiotensin-converting
 DE enzyme inhibitor).
 OS Agkistrodon halys blomhoffii (Mamushi) (Gloydus blomhoffii).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Gloydus.
 OX NCBI_TaxID=242054;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Kato H., Suzuki T.;
 RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
 RT the venom of Agkistrodon halys blomhoffii.";
 RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; A01254; XASNBA.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 6 R 6

RESULT 18

BPP_AGKHP

ID BPP_AGKHP STANDARD; PRT; 11 AA.
AC P04562;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys pallas (Chinese water mocassin) (Gloydius halys
OS pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=86177022; PubMed=3008123;
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
RT "Structure-function studies on the bradykinin potentiating peptide
RT from Chinese snake venom (Agkistrodon halys pallas).";
RL Peptides 6 Suppl. 3:339-342(1985).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; JC0002; XAVIBH.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 3 R 3

RESULT 19

CA21_LITCI

ID CA21_LITCI STANDARD; PRT; 11 AA.
AC P82087;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Caerulein 2.1/2.1Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT montains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry."
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 2.1Y4 differs from isoform 2.1 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1372; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1312 MW; 10DAB7C4EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
 |
 Db 3 D 3

RESULT 20
 CA22_LITCI
 ID CA22_LITCI STANDARD; PRT; 11 AA.
 AC P82088;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 2.2/2.2Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;

RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog *Litoria citropa*. Part 1. Sequence determination
 RT using electrospray mass spectrometry."
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 2.2Y4 differs from isoform 2.2 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1328 MW; 10DAB894EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 D 11
 |
 Db 3 D 3

RESULT 21

CA31_LITCI

ID CA31_LITCI STANDARD; PRT; 11 AA.
 AC P82089;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 3.1/3.1Y4.
 OS *Litoria citropa* (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
 OC Pelodyadinae; *Litoria*.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog *Litoria citropa*. Part 1. Sequence determination
 RT using electrospray mass spectrometry."
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being
 CC sulfated.

CC -!- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 T 4
 |
 Db 6 T 6

RESULT 22

CA32_LITCI

ID CA32_LITCI STANDARD; PRT; 11 AA.
 AC P82090;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 3.2/3.2Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylodea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT montains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry."
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 3.2Y4 differs from isoform 3.2 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1423; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1363 MW; 10DAB8867861A86B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 T 4
|
Db 6 T 6

RESULT 23

CA41_LITCI

ID CA41_LITCI STANDARD; PRT; 11 AA.
AC P82091;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 4.1/4.1Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodryadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT mountains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry."
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 4.1Y4 differs from isoform 4.1 in not being
CC sulfated.
CC -!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1328 MW; 10DAB7C4F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 T 4
|
Db 5 T 5

RESULT 24

CA42_LITCI

ID CA42_LITCI STANDARD; PRT; 11 AA.
 AC P82092;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 4.2/4.2Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry."
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 4.2Y4 differs from isoform 4.2 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 T 4
 |
 Db 5 T 5

RESULT 25

CEP1_ACHFU

ID CEP1_ACHFU STANDARD; PRT; 11 AA.
 AC P22790;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Cardio-excitatory peptide-1 (ACEP-1).
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;

OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Ferussac; TISSUE=Heart atrium;
 RX MEDLINE=90211261; PubMed=2322251;
 RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
 RT "A novel cardio-excitatory peptide isolated from the atria of the
 RT African giant snail, Achatina fulica.";
 RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
 CC -!- FUNCTION: Potentiates the beat of the ventricle, and has also
 CC excitatory actions on the penis retractor muscle, the buccal
 CC muscle and the identified neurons controlling the buccal muscle
 CC movement of achatina.
 CC -!- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
 DR PIR; A34662; A34662.
 KW Hormone; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
 |
 Db 6 R 6

RESULT 26

CORZ_PERAM

ID CORZ_PERAM STANDARD; PRT; 11 AA.
 AC P11496;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Corazonin.
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=89325572; PubMed=2753132;
 RA Veenstra J.A.;
 RT "Isolation and structure of corazonin, a cardioactive peptide from
 RT the American cockroach.";
 RL FEBS Lett. 250:231-234(1989).
 CC -!- FUNCTION: Cardioactive peptide. Corazonin is probably involved
 CC in the physiological regulation of the heart beat.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR; S05002; S05002.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 T 4
|
Db 2 T 2

RESULT 27

COXA_CANFA

ID COXA_CANFA STANDARD; PRT; 11 AA.
AC P99501;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
GN COX5A.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- FUNCTION: This is the heme A-containing chain of cytochrome c
CC oxidase, the terminal oxidase in mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase Va family.
DR HSC-2DPAGE; P99501; DOG.
DR InterPro; IPR003204; Cyt_c_ox5A.
DR Pfam; PF02284; COX5A; 1.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1274 MW; 910B35C5B1AB11F5 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 E 6
|
Db 6 E 6

RESULT 28

CSI5_BACSU

ID CSI5_BACSU STANDARD; PRT; 11 AA.

AC P81095;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cold shock protein CSI5 (11 kDa cold shock protein) (Fragment).
 OS *Bacillus subtilis*.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=168 / JH642;
 RA Graumann P.L., Schmid R., Marahiel M.A.;
 RL Submitted (OCT-1997) to Swiss-Prot.
 RN [2]
 RP CHARACTERIZATION.
 RC STRAIN=168 / JH642;
 RX MEDLINE=96345629; PubMed=8755892;
 RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
 RT "Cold shock stress-induced proteins in *Bacillus subtilis*.";
 RL J. Bacteriol. 178:4611-4619(1996).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- INDUCTION: In response to low temperature.
 CC -!- CAUTION: Could not be found in the genome of *B.subtilis* 168.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1360 MW; 15F6ECEE6322C330 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
 |
 Db 2 R 2

RESULT 29

CX5A_CONAL

ID CX5A_CONAL STANDARD; PRT; 11 AA.
 AC P58848;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Conotoxin au5a.
 OS *Conus aulicus* (Court cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; *Conus*.
 OX NCBI_TaxID=89437;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99452958; PubMed=10521453;
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
 RT "The T-superfamily of conotoxins."
 RL J. Biol. Chem. 274:30664-30671(1999).

RN [2]
 RP ERRATUM.
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
 RL J. Biol. Chem. 274:36030-36030(1999).
 CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is
 CC observed when injected into mice.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1436.6; METHOD=LSIMS.
 CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.
 DR PIR; A59146; A59146.
 KW Toxin.
 FT DISULFID 2 9
 FT DISULFID 3 10
 SQ SEQUENCE 11 AA; 1441 MW; 21A36775440059D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
 |
 Db 7 R 7

RESULT 30

CX5B_CONAL

ID CX5B_CONAL STANDARD; PRT; 11 AA.
 AC P58849;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Conotoxin au5b.
 OS Conus aulicus (Court cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=89437;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99452958; PubMed=10521453;
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
 RT "The T-superfamily of conotoxins."
 RL J. Biol. Chem. 274:30664-30671(1999).
 RN [2]
 RP ERRATUM.
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
 RL J. Biol. Chem. 274:36030-36030(1999).
 CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is
 CC observed when injected into mice (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1388.6; METHOD=LSIMS.
 CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.
 DR PIR; B59146; B59146.
 KW Toxin.
 FT DISULFID 2 9
 FT DISULFID 3 10
 SQ SEQUENCE 11 AA; 1393 MW; 21A36775440042D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
 |
 Db 7 R 7

RESULT 31

CXL1_CONMR

ID CXL1_CONMR STANDARD; PRT; 11 AA.
 AC P58807;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lambda-conotoxin CMrVIA.
 OS Conus marmoreus (Marble cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=42752;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=20564325; PubMed=10988292;
 RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
 RA Seow K.T., Bay B.-H.;
 RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide
 RT pattern and protein folding. Isolation and characterization from the
 RT venom of Conus marmoreus.";
 RL J. Biol. Chem. 275:39516-39522(2000).
 CC -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1237.93; MW_ERR=0.21; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
 KW Neurotoxin; Toxin; Hydroxylation.
 FT DISULFID 2 11
 FT DISULFID 3 8
 FT MOD_RES 10 10 HYDROXYLATION.
 SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
|
Db 6 K 6

RESULT 32

EFG_CLOPA

ID EFG_CLOPA STANDARD; PRT; 11 AA.
AC P81350;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (CP 5) (Fragment).
GN FUSA.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of
CC the nascent protein chain from the A-site to the P-site of the
CC ribosome.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EF-G/EF-2 subfamily.
DR InterPro; IPR000795; EF_GTPbind.
DR PROSITE; PS00301; EFACTOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
|
Db 1 K 1

RESULT 33

FAR6_PENMO

ID FAR6_PENMO STANDARD; PRT; 11 AA.
AC P83321;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP6 (DGRTPALRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Penaeus.
 OX NCBI_TaxID=6687;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RX MEDLINE=21956277; PubMed=11959015;
 RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,
 RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
 RT of the giant tiger prawn *Penaeus monodon*.";
 RL Comp. Biochem. Physiol. 131B:325-337(2002).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=1301.8; METHOD=MALDI.
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
 KW Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1301 MW; 9A19C860072DC771 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
 |
 Db 1 D 1

RESULT 34

FAR9_CALVO
 ID FAR9_CALVO STANDARD; PRT; 11 AA.
 AC P41864;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CalliFMRFamide 9.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thoracic ganglion;
 RX MEDLINE=92196111; PubMed=1549595;
 RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated calliFMRFamides) from the blowfly
 RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 DR PIR; I41978; I41978.
 KW Neuropeptide; Amidation.

FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1359 MW; 8160CE46CAA44321 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
|
Db 5 K 5

RESULT 35

HS70_PINPS
ID HS70_PINPS STANDARD; PRT; 11 AA.
AC P81672;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Heat shock 70 kDa protein (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein
CC (spot N164) is: 5.4, its MW is: 73 kDa.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
KW ATP-binding; Heat shock; Multigene family.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1228 MW; 037C1BE8DAA44DD0 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 E 6
|
Db 2 E 2

RESULT 36

LADD_ONCMY
ID LADD_ONCMY STANDARD; PRT; 11 AA.
AC P81018;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Ladderlectin (Fragment).
 OS *Oncorhynchus mykiss* (Rainbow trout) (*Salmo gairdneri*).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; *Oncorhynchus*.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Blood;
 RX MEDLINE=97293418; PubMed=9149391;
 RA Jensen L.E., Thiel S., Petersen T.E., Jensenuis J.C.;
 RT "A rainbow trout lectin with multimeric structure."
 RL Comp. Biochem. Physiol. 116B:385-390(1997).
 CC -!- FUNCTION: Lectin that binds sepharose.
 CC -!- COFACTOR: Calcium is essential for sepharose binding.
 CC -!- SUBUNIT: Multimeric.
 KW Lectin; Calcium.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1163 MW; 0B26227FF6D45404 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 1 A 1

RESULT 37

LPW_THETH

ID LPW_THETH STANDARD; PRT; 11 AA.
 AC P05624;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Trp operon leader peptide.
 GN TRPL.
 OS *Thermus thermophilus*.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC *Thermus*.
 OX NCBI_TaxID=274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB8 / ATCC 27634;
 RX MEDLINE=89000781; PubMed=2844259;
 RA Sato S., Nakada Y., Kanaya S., Tanaka T.;
 RT "Molecular cloning and nucleotide sequence of *Thermus thermophilus*
 RT HB8 trpE and trpG."
 RL Biochim. Biophys. Acta 950:303-312(1988).
 CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
 CC OF TRYPTOPHAN.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; X07744; CAA30565.1; -.
KW Tryptophan biosynthesis; Leader peptide.
SQ SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 2 A 2

RESULT 38

LSK1_LEUMA

ID LSK1_LEUMA STANDARD; PRT; 11 AA.

AC P04428;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Leucosulfakinin-I (LSK-I).

OS Leucophaea maderae (Madeira cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;

OC Blaberidae; Leucophaea.

OX NCBI_TaxID=6988;

RN [1]

RP SEQUENCE.

RX MEDLINE=86315858; PubMed=3749893;

RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;

RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to

RT gastrin and cholecystokinin.";

RL Science 234:71-73(1986).

CC -!- FUNCTION: Change the frequency and amplitude of contractions of

CC the hingat. Inhibits muscle contraction of hindgut.

CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

DR PIR; A01622; GMROL.

DR InterPro; IPR001651; Gastrin.

DR PROSITE; PS00259; GASTRIN; 1.

KW Hormone; Amidation; Sulfation.

FT MOD_RES 6 6 SULFATION.

FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86B5AAB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 E 6
|
Db 1 E 1

RESULT 39

LSKP_PERAM

ID LSKP_PERAM STANDARD; PRT; 11 AA.
AC P36885;
DT 01-JUN-1994 (Rel. 29, Created).
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Perisulfakinin (Pea-SK-I).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90137190; PubMed=2615921;
RA Veenstra J.A.;
RT "Isolation and structure of two gastrin/CCK-like neuropeptides from
RT the American cockroach homologous to the leucosulfakinins."
RL Neuropeptides 14:145-149(1989).
CC -!- FUNCTION: Stimulates hindgut contractions.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A60656; A60656.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Hormone; Amidation; Sulfation.
FT MOD_RES 6 6 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAA CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 E 6
|
Db 1 E 1

RESULT 40

MHBI_KLEPN

ID MHBI_KLEPN STANDARD; PRT; 11 AA.
AC P80580;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Maleylpyruvate isomerase (EC 5.2.1.4) (Fragment).
GN MHBI.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE.
RX MEDLINE=96349117; PubMed=8760924;
RA Robson N.D., Parrott S., Cooper R.A.;

RT "In vitro formation of a catabolic plasmid carrying Klebsiella
 RT pneumoniae DNA that allows growth of Escherichia coli K-12 on 3-
 RT hydroxybenzoate.";
 RL Microbiology 142:2115-2120(1996).
 CC -!- CATALYTIC ACTIVITY: 3-maleylpyruvate = 3-fumarylpyruvate.
 KW Isomerase.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1387 MW; 1EE0E2DD49C9D5AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
 |
 Db 2 K 2

RESULT 41
 MLG_THETS

ID MLG_THETS STANDARD; PRT; 11 AA.
 AC P41989;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Melanotropin gamma (Gamma-melanocyte stimulating hormone) (Gamma-MSH).
 OS Theromyzon tessulatum (Leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
 OX NCBI_TaxID=13286;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=94298944; PubMed=8026574;
 RA Salzet M., Wattez C., Bulet P., Malecha J.;
 RT "Isolation and structural characterization of a novel peptide related
 RT to gamma-melanocyte stimulating hormone from the brain of the leech
 RT Theromyzon tessulatum.";
 RL FEBS Lett. 348:102-106(1994).
 CC -!- SIMILARITY: Belongs to the POMC family.
 DR PIR; S45698; S45698.
 KW Hormone; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1486 MW; 2DB8FACE6409C1E8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
 |
 Db 7 R 7

RESULT 42

NUHM_CANFA
 ID NUHM_CANFA STANDARD; PRT; 11 AA.

AC P49820;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)
 DE (EC 1.6.99.3) (Fragment).
 GN NDUFV2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
 CC TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)
 CC FRAGMENT OF THE ENZYME.
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
 CC -!- COFACTOR: Binds 1 2Fe-2S cluster (Potential).
 CC -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
 CC -!- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the
 CC mitochondrial inner membrane.
 CC -!- SIMILARITY: Belongs to the complex I 24 kDa subunit family.
 DR HSC-2DPAGE; P49820; DOG.
 DR InterPro; IPR002023; Cmplx1_24kDa.
 DR PROSITE; PS01099; COMPLEX1_24K; PARTIAL.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;
 KW Iron-sulfur; Iron; 2Fe-2S.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DD8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A 1
 |
 Db 2 A 2

RESULT 43

NXSN_PSETE

ID NXSN_PSETE STANDARD; PRT; 11 AA.

AC P59072;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Short neurotoxin N1 (Alpha neurotoxin) (Fragment).

OS Pseudonaja textilis (Eastern brown snake).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophiinae; Pseudonaja.
 OX NCBI_TaxID=8673;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99449602; PubMed=10518793;
 RA Gong N.L., Armugam A., Jeyaseelan K.;
 RT "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA
 RT cloning, expression and protein characterization.";
 RL Eur. J. Biochem. 265:982-989(1999).
 CC -!- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
 CC acetylcholine receptors (nAChR).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- MASS SPECTROMETRY: MW=6236; METHOD=Electrospray.
 CC -!- MISCELLANEOUS: LD(50) is 0.84 mg/kg by intravenous injection.
 CC -!- SIMILARITY: Belongs to the snake toxin family.
 DR InterPro; IPR003571; Snake_toxin.
 DR PROSITE; PS00272; SNAKE_TOXIN; PARTIAL.
 KW Toxin; Neurotoxin; Postsynaptic neurotoxin;
 KW Acetylcholine receptor inhibitor; Multigene family.
 FT UNSURE 3 3
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1319 MW; 0D1EF0C81B58732B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 T 4
 |
 Db 2 T 2

RESULT 44

OAIF_SARBU

ID OAIF_SARBU STANDARD; PRT; 11 AA.
 AC P83518;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ovary-derived ACE interactive factor (Neb-ODAIF) [Contains: Neb-
 DE ODAIF(1-9); Neb-ODAIF(1-7)].
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Sarcophagidae; Sarcophaga.
 OX NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND MASS SPECTROMETRY.
 RC TISSUE=Ovary;
 RX MEDLINE=22272747; PubMed=12383874;
 RA Vandingenen A., Hens K., Baggerman G., Macours N., Schoofs L.,
 RA De Loof A., Huybrechts R.;
 RT "Isolation and characterization of an angiotensin converting enzyme
 RT substrate from vitellogenic ovaries of Neobellieria bullata.";

RL Peptides 23:1853-1863(2002).
 CC -!- FUNCTION: Substrate for angiotensin converting enzyme (ACE) in
 CC vitro.
 CC -!- PTM: ACE hydrolyzes Neb-ODAIF by sequentially cleaving off two C-
 CC terminal dipeptides.
 CC -!- MASS SPECTROMETRY: MW=1312.7; METHOD=MALDI; RANGE=1-11.
 CC -!- SIMILARITY: To the N-terminal part of insect vitellogenins.
 FT PEPTIDE 1 11 NEB-ODAIF.
 FT PEPTIDE 1 9 NEB-ODAIF(1-9).
 FT PEPTIDE 1 7 NEB-ODAIF(1-7).
 SQ SEQUENCE 11 AA; 1314 MW; 4E114BB566C5A763 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
 |
 Db 2 K 2

RESULT 45

PKC1_CARMO

ID PKC1_CARMO STANDARD; PRT; 11 AA.
 AC P82684;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-1 (Cam-PK-1) (FXPRL-Amide).
 OS Carausius morosus (Indian stick insect).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatodea;
 OC Heteronemiidae; Carausius.
 OX NCBI_TaxID=7022;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Corpora cardiaca;
 RA Predel R., Kellner R., Gaede G.;
 RT "Myotropic neuropeptides from the retrocerebral complex of the stick
 RT insect, Carausius morosus (Phasmatodea: Lonchodidae).";
 RL Eur. J. Entomol. 96:275-278(1999).
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 CC activity).
 CC -!- MASS SPECTROMETRY: MW=1235; METHOD=MALDI.
 CC -!- SIMILARITY: Belongs to the pyrokinin family.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1236 MW; 2BFA5225BB46C1A8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 E 6
 |

Db

2 E 2

RESULT 46

PQQC_PSEFL

ID PQQC_PSEFL STANDARD; PRT; 11 AA.
 AC P55173;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Coenzyme PQQ synthesis protein C (Pyrroloquinoline quinone
 biosynthesis protein C) (Fragment).
 GN PQQC.
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHA0;
 RX MEDLINE=96064397; PubMed=8526497;
 RA Schnider U., Keel C., Defago G., Haas D.;
 RT "Tn5-directed cloning of pqq genes from Pseudomonas fluorescens CHA0:
 RT mutational inactivation of the genes results in overproduction of the
 RT antibiotic pyoluteorin.";
 RL Appl. Environ. Microbiol. 61:3856-3864(1995).
 CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
 CC -!- SIMILARITY: Belongs to the pqqC family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X87299; CAA60734.1; -.
 DR PIR; S58244; S58244.
 DR HAMAP; MF_00654; -; 1.
 KW PQQ biosynthesis.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1182 MW; 89DF46E4C5B73771 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 9e+04;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 T 4

|

Db 2 T 2

RESULT 47

PVK1_PERAM

ID PVK1_PERAM STANDARD; PRT; 11 AA.
 AC P41837;

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Periviscerokinin-1 (Pea-PVK-1).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Abdominal perisymphathetic organs;
 RX MEDLINE=95232021; PubMed=7716075;
 RA Predel R., Linde D., Rapus J., Vettermann S., Penzlin H.;
 RT "Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the
 RT perisymphathetic organs of the American cockroach.";
 RL Peptides 16:61-66(1995).
 CC -!- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE
 CC HYPERNEURAL MUSCLE.
 KW Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1114 MW; 39DB5419D7605728 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 2 A 2

RESULT 48

RANC_RANPI

ID RANC_RANPI STANDARD; PRT; 11 AA.
 AC P08951;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranatensin-C.
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8404;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=84131098; PubMed=6141890;
 RA Nakajima T.;
 RL Unpublished results, cited by:
 RL Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;
 RL Comp. Biochem. Physiol. 77C:99-108(1984).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin
 CC family.
 DR InterPro; IPR000874; Bombesin.

DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Amphibian defense peptide; Bombesin family; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1304 MW; D6C9885A61ADC366 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 T 4
|
Db 2 T 2

RESULT 49

RE41_LITRU

ID RE41_LITRU STANDARD; PRT; 11 AA.
AC P82074;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Rubellidin 4.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australin red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1039; METHOD=FAB.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1040 MW; 84ED5CBC2877205A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
|
Db 4 D 4

RESULT 50

RRPL_CHAV

ID RRPL_CHAV STANDARD; PRT; 11 AA.
AC P13179;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
DE (L protein) (Fragment).
GN L.
OS Chandipura virus (strain I653514).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Vesiculovirus.
OX NCBI_TaxID=11273;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89299473; PubMed=2741347;
RA Masters P.S., Bhella R.S., Butcher M., Patel B., Ghosh H.P.,
RA Banerjee A.K.;
RT "Structure and expression of the glycoprotein gene of Chandipura
RT virus.";
RL Virology 171:285-290(1989).
CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
CC POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS
CC METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).
CC -!- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE
CC NUCLEOCAPSID (N) PROTEIN.
CC -!- SIMILARITY: WITH THE L PROTEIN OF OTHER RHABDOVIRUSES AND
CC PARAMYXOVIRUSES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J04350; AAA42917.1; -.
KW Transferase; RNA-directed RNA polymerase.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1189 MW; 0335D6E3AAB2D764 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
|
Db 2 D 2

RESULT 51
T2P1_PROVU
ID T2P1_PROVU STANDARD; PRT; 11 AA.
AC P31031;
DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Type II restriction enzyme PvuI (EC 3.1.21.4) (Endonuclease PvuI)
 DE (R.PvuI) (Fragment).
 GN PVUIR.
 OS *Proteus vulgaris*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Proteus*.
 OX NCBI_TaxID=585;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13315;
 RX MEDLINE=93087186; PubMed=1454536;
 RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
 RT "Cloning and characterization of genes for the PvuI restriction and
 RT modification system."
 RL Nucleic Acids Res. 20:5743-5747(1992).
 CC -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
 CC CLEAVES AFTER T-4.
 CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
 CC specific double-stranded fragments with terminal 5'-phosphates.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L04163; AAA25660.1; -.
 DR PIR; S35490; S35490.
 DR REBASE; 1541; PvuI.
 KW Restriction system; Hydrolase; Nuclease; Endonuclease.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 S 9
 |
 Db 2 S 2

RESULT 52

TIN1_HOPTI

ID TIN1_HOPTI STANDARD; PRT; 11 AA.

AC P82651;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Tigerinin-1.

OS *Hoplobatrachus tigerinus* (Indian bull frog) (*Rana tigerina*).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;

OC Hoplobatrachus.
 OX NCBI_TaxID=103373;
 RN [1]
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
 RC TISSUE=Skin secretion;
 RX PubMed=11031261;
 RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
 RA Devi A.S., Nagaraj R., Sitaram N.;
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
 RT tigerina.";
 RL J. Biol. Chem. 276:2701-2707(2001).
 CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
 CC S.aureus, M.luteus, P.putida and S.cerevisiae.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- MASS SPECTROMETRY: MW=1342; METHOD=MALDI.
 KW Amphibian defense peptide; Antibiotic; Fungicide; Amidation.
 FT DISULFID 2 10
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 T 4
 |
 Db 3 T 3

RESULT 53

TIN4_HOPTI
 ID TIN4_HOPTI STANDARD; PRT; 11 AA.
 AC P82654;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tigerinin-4.
 OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
 OC Hoplobatrachus.
 OX NCBI_TaxID=103373;
 RN [1]
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
 RC TISSUE=Skin secretion;
 RX PubMed=11031261;
 RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
 RA Devi A.S., Nagaraj R., Sitaram N.;
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
 RT tigerina.";
 RL J. Biol. Chem. 276:2701-2707(2001).
 CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
 CC S.aureus, M.luteus, P.putida and S.cerevisiae.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.

KW Amphibian defense peptide; Antibiotic.
FT DISULFID 3 11
SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
|
Db 1 R 1

RESULT 54

TKC2_CALVO
ID TKC2_CALVO STANDARD; PRT; 11 AA.
AC P41518;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Callitachykinin II.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95075727; PubMed=7984492;
RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
RA Naessel D.R.;
RT "Callitachykinin I and II, two novel myotropic peptides isolated from
RT the blowfly, Calliphora vomitoria, that have resemblances to
RT tachykinins.";
RL Peptides 15:761-768(1994).
CC -!- FUNCTION: Myoactive peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1103 MW; 15D7E3F9C9CDD444 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 6 A 6

RESULT 55

TKN1_PSEGU
ID TKN1_PSEGU STANDARD; PRT; 11 AA.
AC P42986;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kassinin-like peptide K-I (PG-KI).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylaidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guentheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; B60409; B60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 D 11
 |
 Db 5 D 5

RESULT 56

TKN1_UPEIN
 ID TKN1_UPEIN STANDARD; PRT; 11 AA.
 AC P82026;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Uperin 1.1.
 OS Uperoleia inundata (Floodplain toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylaidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=104953;

RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 RA Adams G.W., Severini C.;
 RT "Novel uperin peptides from the dorsal glands of the Australian
 RT floodplain toadlet *Uperoleia inundata*.";
 RL Aust. J. Chem. 49:475-484(1996).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=1208; METHOD=FAB.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1226 MW; 3293693E59CDD457 CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 A 1
 |
 Db 2 A 2

RESULT 57
 TKN1_UPERU
 ID TKN1_UPERU STANDARD; PRT; 11 AA.
 AC P08612;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Uperolein.
 OS *Uperoleia rugosa* (Wrinkled toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; *Uperoleia*.
 OX NCBI_TaxID=8368;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=75131227; PubMed=1120493;
 RA Anastasi A., Erspamer V., Endean R.;
 RT "Structure of uperolein, a physalaemin-like endecapeptide occurring
 RT in the skin of *Uperoleia rugosa* and *Uperoleia marmorata*.";
 RL Experientia 31:394-395(1975).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and

CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
 |
 Db 3 D 3

RESULT 58

TKN2_PSEGU

ID TKN2_PSEGU STANDARD; PRT; 11 AA.
 AC P42987;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kassinin-like peptide K-II (PG-KII).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guentheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; C60409; C60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.

DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
 |
 Db 5 D 5

RESULT 59

TKN3_PSEGU

ID TKN3_PSEGU STANDARD; PRT; 11 AA.
 AC P42988;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kassinin-like peptide K-III (PG-KIII).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guntheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; D60409; D60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 E 6
|
Db 6 E 6

RESULT 60

TKN4_PSEGU

ID TKN4_PSEGU STANDARD; PRT; 11 AA.

AC P42989;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Substance P-like peptide I (PG-SPI).

OS Pseudophryne guentheri (Guenther's toadlet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;

OC Myobatrachinae; Pseudophryne.

OX NCBI_TaxID=30349;

RN [1]

RP SEQUENCE.

RC TISSUE=Skin secretion;

RX MEDLINE=90287814; PubMed=2356157;

RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,

RA Roberts J.D., Melchiorri P., Erspamer V.;

RT "Six novel tachykinin- and bombesin-related peptides from the skin of
the Australian frog Pseudophryne guentheri.";

RL Peptides 11:299-304(1990).

CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.

CC -!- SIMILARITY: Belongs to the tachykinin family.

DR PIR; E60409; E60409.

DR InterPro; IPR002040; Tachy_Neurokinin.

DR InterPro; IPR008215; Tachykinin.

DR Pfam; PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.

DR PROSITE; PS00267; TACHYKININ; 1.

KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;

KW Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11

Db

5 D 5

RESULT 61

TKN5_PSEGU

ID TKN5_PSEGU STANDARD; PRT; 11 AA.
AC P42990;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide II (PG-SPII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyla; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; F60409; F60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 E 6
|
Db 6 E 6

RESULT 62

TKNA_CHICK

ID TKNA_CHICK STANDARD; PRT; 11 AA.

AC P19850;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=88204263; PubMed=2452461;
 RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
 RT "[Arg3]substance P and neurokinin A from chicken small intestine.";
 RL Regul. Pept. 20:171-180(1988).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; JN0023; JN0023.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
 |
 Db 1 R 1

RESULT 63

TKNA_GADMO

ID TKNA_GADMO STANDARD; PRT; 11 AA.
 AC P28498;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Gadus morhua (Atlantic cod).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
 OX NCBI_TaxID=8049;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92298992; PubMed=1376687;

RA Jensen J., Conlon J.M.;
 RT "Substance-P-related and neurokinin-A-related peptides from the brain
 RT of the cod and trout."
 RL Eur. J. Biochem. 206:659-664(1992).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S23306; S23306.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
 SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
 |
 Db 1 K 1

RESULT 64

TKNA_HORSE

ID TKNA_HORSE STANDARD; PRT; 11 AA.
 AC P01290;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Equus caballus (Horse), and
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796, 10141;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Horse;
 RA Studer R.O., Trzeciak A., Lergier W.;
 RT "Isolation and amino-acid sequence of substance P from horse
 RT intestine."
 RL Helv. Chim. Acta 56:860-866(1973).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=C.porcellus;
 RX MEDLINE=90044685; PubMed=2478925;
 RA Murphy R.;
 RT "Primary amino acid sequence of guinea-pig substance P."
 RL Neuropeptides 14:105-110(1989).

CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; A01558; SPHO.
 DR PIR; A60654; A60654.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
 |
 Db 1 R 1

RESULT 65

TKNA_ONCMY

ID TKNA_ONCMY STANDARD; PRT; 11 AA.
 AC P28499;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92298992; PubMed=1376687;
 RA Jensen J., Conlon J.M.;
 RT "Substance-P-related and neurokinin-A-related peptides from the brain
 RT of the cod and trout."
 RL Eur. J. Biochem. 206:659-664(1992).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S23308; S23308.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
 SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
 |
 Db 1 K 1

RESULT 66

TKNA_RANCA

ID TKNA_RANCA STANDARD; PRT; 11 AA.

AC P22688;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ranatachykinin A (RTK A).

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OX NCBI_TaxID=8400;

RN [1]

RP SEQUENCE, AND SYNTHESIS.

RC TISSUE=Brain, and Intestine;

RX MEDLINE=91254337; PubMed=2043143;

RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;

RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)

RT brain and intestine.";

RL Biochem. Biophys. Res. Commun. 177:588-595(1991).

RN [2]

RP SEQUENCE.

RC TISSUE=Intestine;

RX MEDLINE=94023216; PubMed=8210506;

RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;

RT "Four novel tachykinins in frog (Rana catesbeiana) brain and

RT intestine.";

RL Regul. Pept. 46:81-88(1993).

CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the tachykinin family.

DR PIR; A61033; A61033.

DR InterPro; IPR002040; Tachy_Neurokinin.

DR InterPro; IPR008215; Tachykinin.

DR Pfam; PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.

DR PROSITE; PS00267; TACHYKININ; 1.

KW Tachykinin; Neuropeptide; Amidation.

FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1311 MW; 200D60CC59D40AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3

Db 1 K 1

RESULT 67

TKNA_SCYCA

ID TKNA_SCYCA STANDARD; PRT; 11 AA.
AC P41333;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=93292508; PubMed=7685693;
RA Waugh D., Wang Y., Hazon N., Balment R.J., Conlon J.M.;
RT "Primary structures and biological activities of substance-P-related
peptides from the brain of the dogfish, Scyliorhinus canicula.";
RL Eur. J. Biochem. 214:469-474(1993).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S33300; S33300.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D867 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3

Db 1 K 1

RESULT 68

TKN_PHYFU

ID TKN_PHYFU STANDARD; PRT; 11 AA.

AC P08615;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Physalaemin.
 OS Physalaemus fuscumaculatus (Neotropical frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;
 OC Leptodactylinae; Physalaemus.
 OX NCBI_TaxID=8378;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=66076612; PubMed=5857249;
 RA Erspamer V., Anastasi A., Bertaccini G., Cei J.M.;
 RT "Structure and pharmacological actions of physalaemin, the main
 RT active polypeptide of the skin of Physalaemus fuscumaculatus.";
 RL Experientia 20:489-490(1964).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S07201; S07201.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1283 MW; 3293693E59C33457 CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 A 1
 |
 Db 2 A 2

RESULT 69

UF05_MOUSE

ID UF05_MOUSE STANDARD; PRT; 11 AA.
 AC P38643;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P48) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE.
 RC TISSUE=Fibroblast;
 RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familiar and novel murine proteins
 RT using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 5.5, its MW is: 48 kDa.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1328 MW; E54835E5CAAABAFa CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3
 |
 Db 1 K 1

RESULT 70

ULAG_HUMAN

ID ULAG_HUMAN STANDARD; PRT; 11 AA.
 AC P31933;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of liver tissue (Spot 118) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=94147969; PubMed=8313870;
 RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
 RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
 RT "Human liver protein map: update 1993.";
 RL Electrophoresis 14:1216-1222(1993).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 5.5, its MW is: 34 kDa.
 DR SWISS-2DPAGE; P31933; HUMAN.
 DR Siena-2DPAGE; P31933; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1219 MW; EDABD37F272DDB0A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 E 6
 |
 Db 5 E 5

Search completed: April 8, 2004, 15:47:21
Job time : 6.15385 secs